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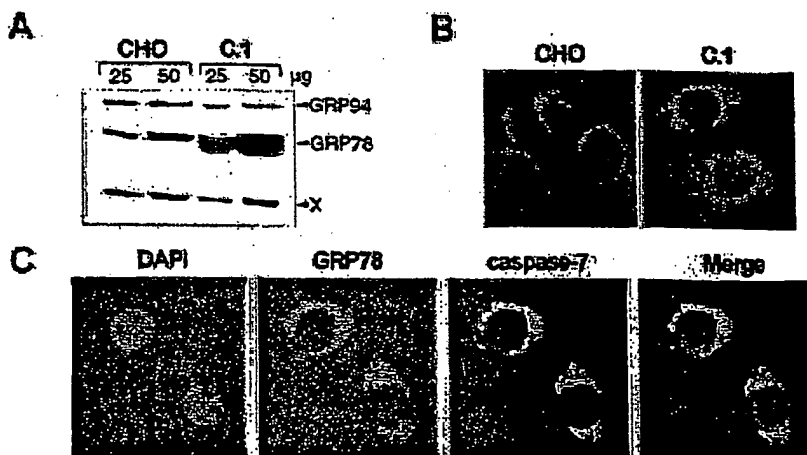
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(54) Title: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS



(57) Abstract: This invention relates to compositions and methods for modulating apoptosis by regulating the activity of endoplasmic reticulum transmembrane glucose regulated protein 78 (GRP78).

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Methods and Compositions for Modulating Apoptosis

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority under 35 U.S.C. §119 to U.S. Provisional Application Serial No. 60/514,661, filed October 27, 2003, the disclosure of which is incorporated herein by reference.

STATEMENT AS TO FEDERALLY-SPONSORED RESEARCH

[0002] Pursuant to 35 U.S.C. §202(c), it is acknowledged that the U.S. Government has certain rights in the invention described herein, which was made in part with funds from the National Institutes of Health, Grant Nos. CA 20607 and AI42394.

TECHNICAL FIELD

[0003] This invention relates to methods and compositions for modulating apoptosis by selectively targeting glucose regulated proteins (GRPs) and more particularly to modulating the activity and/or interaction of GRP78 and procaspase.

BACKGROUND

[0004] Resistance to chemotherapy remains a major obstacle for the treatment of cancer. The complexity of drug resistance in human cancer strongly suggests the involvement of multiple pathways. One mechanism, both intrinsic and acquired, is the result of genetic alterations within cancer cells. Another mechanism may result from environmental conditions that occur naturally in solid tumors. Because of poor vascularization, solid tumors usually contain regions undergoing glucose starvation and hypoxia, resulting in acidosis and alterations in cell metabolism. These pockets of hypoxia and nutrient deprivation occur in well differentiated, slow growing, non-metastatic tumors, as well as in rapidly growing, aggressive anaplastic malignancies.

[0005] Stress conditions in cell culture, such as glucose starvation, commonly cause the glucose-regulated stress response which, is part of a general cellular defense mechanism referred to as the unfolded protein response (UPR). One characteristic of the UPR is the induction of the endoplasmic reticulum (ER) resident stress proteins referred to as the glucose-regulated

proteins (GRPs). The GRPs are Ca^{2+} -binding chaperone proteins with protective properties. The best characterized GRP is GRP78, a 78-kDa protein also referred to as BiP. As a protein chaperone, GRP78 is known to form complexes with heterologous proteins that are processed through the ER.

[0006] Glucose Regulated Proteins, or GRPs (GRP74, GRP78, GRP94, GRP170, ERp72, PDI, calreticulin, and GRP58 (alias ERp57)) are ER molecular chaperones that assist in protein folding and assembly. GRP78, GRP94, ERp72 and calreticulin are also Ca^{2+} binding proteins. GRP78 and GRP94 share sequence homology with heat shock proteins. The GRP family of proteins is coordinately induced by glucose starvation, anoxia, alterations in intracellular calcium and, exposure to inhibitors of glycosylation as well as by PDT-mediated oxidative stress (Gomer, et al., Cancer Res. 51:6574-79, 1991; and Li, et al., J. Cell Physiol. 153:575-82, 1992). The 78,000 GRP (i.e., GRP78) is identical in sequence to the immunoglobulin heavy chain binding protein and both GRP78 and GRP94 are localized in the ER.

[0007] Many of the cytotoxic drugs, including topoisomerase inhibitors such as etoposide, initiate programmed cell death. DNA damaging agents such as etoposide can trigger cell death through the p53-mediated caspase cell death signaling cascade, resulting in cytochrome c release and the activation of caspase-3. Caspases-3, -6, and -7 are members of the apoptotic executing group of caspases with caspase-7 structurally and functionally most similar to caspase-3. Active caspase-7 has been shown to be associated with the mitochondria and the ER membranes, whereas caspase-3 remains cytosolic. Although these observations suggest that similar apoptotic executioner's function in different cellular compartments and act on distinct substrates, there is limited information on the contribution of organelles such as the ER in the apoptotic process.

[0008] Accordingly, there exists a need in the art to identify key interactions between proteins involved in the apoptotic pathway and to regulate those interactions.

SUMMARY

[0009] Overexpression and antisense approaches in cell systems show that GRP78 can protect cells against cell death caused by disturbance of ER homeostasis. Whereas GRP78 overexpression could limit damage in normal tissues and organs exposed to ER stress, the anti-apoptotic function of GRP78 also predicts that its natural induction in neoplastic cells could lead to cancer progression and drug resistance. In a variety of cancer cell lines, solid tumors, and human cancer biopsies, the level of GRP78 is elevated, correlating with malignancy. Using human cancer and other cell lines, a large number of stress induction studies show that a glucose-regulated stress response results in the induction of GRP78 and other coordinately regulated GRP genes correlating with cellular drug resistance. Nonetheless, the direct role of GRPs in conferring drug resistance has not been proven. This is because of the inherent problems associated with using stress inducers or deficiencies in certain cell functions to induce the GRPs, because the inducing conditions can exert other unknown pleiotropic effects, possibly affecting multiple cellular pathways. Furthermore, the mechanisms for the protective function of the ER localized GRPs in drug resistance are not understood.

[0010] Methods and compositions for modulating apoptosis by regulating the physical and functional interactions of glucose responsive protein 78 (GRP78) with cytosolic components of a cell that mediate apoptosis are provided. The methods and compositions are particularly well suited to identifying agents that can be used in conjunction with apoptosis-inducing therapeutic compounds to treat cell proliferative disorders. Thus, the disclosure relates to the preparation of pharmaceutical compositions for treating, preventing, and/or delaying a disease in a subject, such as, for example, a cell proliferative disorder.

[0011] Accordingly, in one embodiment, the invention provides a method of modulating apoptosis by contacting glucose regulated protein 78 (GRP78) endoplasmic reticulum transmembrane protein with an agent that regulates the interaction of the transmembrane protein with a cytosolic component that mediates apoptosis. In

one aspect, the cytosolic component is a caspase. The caspase can be, for example, caspase-7. In general, the method can be used to promote or inhibit apoptosis. The agent can be, for example, a polypeptide, an antibody or a small molecule. In one aspect, the agent interacts with the ATP-binding domain of GRP78.

[0012] In another embodiment, the invention provides a method of modulating apoptosis by contacting glucose regulated protein 78 (GRP78) with an agent that inhibits or prevents the ability of the protein to integrate in to the membrane of the endoplasmic reticulum. In one aspect, the agent interacts with a hydrophobic transmembrane domain III (amino acids 210-260 of SEQ ID NO:2) or domain IV (amino acids 400-450 of SEQ ID NO:2) of GRP78.

[0013] In a further embodiment, the invention provides a method of identifying an agent that modulates the interaction of glucose regulated protein 78 (GRP78) with a cytosolic component that mediates apoptosis. The method includes providing glucose regulated protein 78 (GRP78) integrally-associated with a membrane, providing a cytosolic component comprising at least one caspase, providing an agent, contacting the protein with the component and the agent simultaneously or in succession, and determining the effect of the agent on the interaction of the protein and the component as compared to a control.

[0014] In a further embodiment, the invention provides a method of identifying an agent that modulates the interaction of glucose regulated protein 78 (GRP78) with a membrane. The method includes providing a polypeptide comprising the hydrophobic transmembrane domain III (amino acids 210-260 of SEQ ID NO:2) and/or domain IV (amino acids 400-450 of SEQ ID NO:2) of the protein of glucose regulated protein 78 (GRP78), providing an agent, contacting the polypeptide with the agent, and determining the effect of the agent on the ability of the polypeptide to incorporate in to the membrane, as compared to a control.

[0015] In yet another embodiment, the invention provides a method of inhibiting apoptosis in a target tissue by overexpressing GRP78 or GRP94 in said tissue. Exemplary tissues include neuronal tissue, vascular tissue and cardiac tissue.

[0016] The invention provides a method of modulating apoptosis in a cell, the method comprising contacting a glucose

regulated protein (GRP) with an agent that regulates the interaction of the GRP with a cytosolic component that mediates apoptosis.

[0017] The invention also provides a method of promoting apoptosis in a cell, the method comprising inhibiting glucose regulated protein 78 (GRP78) with an agent that (i) inhibits or prevents the ability of GRP78 to interact with a cytosolic protein and/or (ii) inhibits the production of GRP78.

[0018] The invention further provides a method of identifying an agent that modulates the interaction of glucose regulated protein 78 (GRP78) with a cytosolic component that mediates apoptosis. The method comprises (a) providing glucose regulated protein 78 (GRP78) integrally-associated with a membrane; (b) providing a cytosolic component comprising at least one caspase; (c) providing an agent; (d) contacting the protein of a) with the component of (b) and the agent of (c) simultaneously or in succession; and (e) determining the effect of the agent on the interaction of the protein and the component as compared to a control.

[0019] The invention provides a glucose regulated protein (GRP) inhibitory nucleic acid molecule comprising a nucleic acid that interacts with a glucose regulated protein (GRP) polynucleotide. In one aspect, the inhibitory nucleic acid is an antisense molecule. In another aspect, the nucleic acid is a small inhibitory nucleic acid (siNA) molecule.

[0020] The invention also provides a glucose regulated protein modulating agent comprising a soluble domain of a GRP protein.

[0021] The invention further provides a method of identifying an agent that modulates the interaction of glucose regulated protein 78 (GRP78) with a cytosolic component that mediates apoptosis, the method comprising: (a) providing a polypeptide comprising the ATP-binding domain of glucose regulated protein 78 (GRP78); (b) providing a cytosolic component comprising at least one caspase; (c) providing an agent; (d) contacting the polypeptide of a) with the component of (b) and the agent of (c) simultaneously or in succession; and (f) determining the effect

of the agent on the interaction of the polypeptide and the component as compared to a control.

[0022] The invention yet further provides a method of identifying an agent that modulates the interaction of glucose regulated protein 78 (GRP78) with a membrane, the method comprising: (a) providing a polypeptide comprising the hydrophobic transmembrane domain III (amino acids 210-260 of SEQ ID NO:1 or 2) and/or domain IV (amino acids 400-450 of SEQ ID NO:1 or 2) of the protein of glucose regulated protein 78 (GRP78); (b) providing an agent; (c) contacting the polypeptide of a) the agent of b) simultaneously or in succession; and (d) determining the effect of the agent on the interaction of the polypeptide with the membrane as compared to a control.

[0023] The invention provides a method of modulating apoptosis, the method comprising contacting a cell comprising a caspase polypeptide with an agent that regulates the interaction of the polypeptide with glucose regulated protein 78 (GRP78) endoplasmic reticulum transmembrane protein.

[0024] The invention also provides a method of modulating apoptosis, the method comprising contacting a cell comprising a glucose regulated protein 94 (GRP94) endoplasmic reticulum transmembrane protein with an agent that regulates the interaction of the transmembrane protein with a cytosolic component that mediates apoptosis.

[0025] The invention further provides a method of inhibiting apoptosis in a target tissue, the method comprising overexpressing GRP78 or GRP94 in said tissue.

[0026] The invention provides a method of identifying an agent that modulates the interaction of glucose regulated protein 94 (GRP94) with a cytosolic component that mediates apoptosis, the method comprising: (a) providing glucose regulated protein 94 (GRP94); (b) providing a cytosolic component comprising at least one caspase; (c) providing an agent; (d) contacting the protein of (a) with the component of (b) and the agent of (c) simultaneously or in succession; and (e) determining the effect of the agent on the interaction of the protein and the component as compared to a control.

[0027] Also provided by the invention is a nucleic acid construct comprising a glucose regulated protein (GRP) inhibitory nucleic acid molecule operably linked to an expression control element.

[0028] In another aspect, the invention provides a recombinant vector comprising a nucleic acid construct comprising a glucose regulated protein (GRP) inhibitory nucleic acid molecule operably linked to an expression control element.

[0029] The invention provides a pharmaceutical composition comprising a nucleic acid construct of the invention in a pharmaceutically acceptable carrier.

[0030] A method for inhibiting cell proliferation is also provided by the invention. The method comprising contacting a target cell having a cell proliferative disorder with a nucleic acid construct of the invention.

[0031] In yet another aspect the invention provides a method for treating a cell proliferative disorder in a subject comprising administering to the subject a nucleic acid construct of the invention.

[0032] The invention provides a nucleic acid construct comprising a glucose regulated protein (GRP) polynucleotide operably linked to an expression control element.

[0033] The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

DESCRIPTION OF DRAWINGS

[0034] **Figure 1, Panel A** depicts a comparison of GRP78 protein levels in parental CHO cell line and its derivative C.1. Total protein lysates (25 and 50 µg/lane) were separated on 8% SDS-PAGE, and the levels of GRP78, GRP94, and protein X were determined by immunoblotting with an anti-KDEL antibody.

[0035] **Figure 1, Panel B** depicts GRP78 localization by immunofluorescence. Subcellular distribution of GRP78 is primarily perinuclear, indicative of ER localization.

[0036] **Figure 1, Panel C** depicts co-localization of GRP78 and caspase-7 in the ER. Green fluorescence indicates caspase-7, red

indicates GRP78, and purple staining represents the nucleus. In the merged images, yellow staining indicates co-localization.

[0037] Figure 2, Panel A depicts clonogenic survival assays for CHO and C.1 cells subjected to various concentrations of etoposide for 6 h.

[0038] Figure 2, Panel B depicts clonogenic survival assays for CHO and C.1 cells subjected to various concentrations of adriamycin for 1 h.

[0039] Figure 2, Panel C depicts clonogenic survival assays for CHO and C.1 cells subjected to various concentrations of camptothecin for 24 h.

[0040] Figure 3, Panel A depicts GRP78 overexpression protecting cells from etoposide-induced apoptosis. C.1 and CHO cells were either non-treated (Ctrl) or treated with 30 μ M etoposide (Etop) for 6 h. Viable cells are those with low annexin or no annexin and PI staining (lower left panel). Early stage apoptotic cells are represented by high annexin and low PI staining (lower right panel), later stage apoptotic cells represented by high annexin and high PI staining (upper right panel), and necrosis is represented by cells with high PI and low annexin staining (upper left panel).

[0041] Figure 3, Panel B depicts DNA fragmentation pattern of CHO and C.1 cells following etoposide treatment.

[0042] Figure 4, Panel A depicts overexpression of GRP78 confers etoposide resistance to human bladder carcinoma T24/83 cells. T24/83 cell lines stably transfected with the empty vector pcDNA (T24/83-pcDNA) or vector expressing wild-type GRP78 (T24/83-GRP78) were established. Immunoblot analysis of GRP78 protein level for the two cell lines is shown (inset).

[0043] Figure 4, Panel B depicts immunofluorescence imaging of GRP78 expression in T24/83 cells. GRP78 localization is perinuclear.

[0044] Figure 4, Panel C depicts the effect of overexpression of GRP78 on etoposide-induced apoptosis. T24/83-pcDNA and T24/83-GRP78 cells were either non-treated (Ctrl) or treated with etoposide (Etop).

[0045] Figure 5, Panel A depicts the effect of GRP78 overexpression on topoisomerase II expression and caspase-7

activation. Total protein lysates were prepared from non-treated (Ctrl) or etoposide-treated (Etop) CHO and C.1 cells.

[0046] Figure 5, Panel B depicts overexpression of GRP78 as inhibiting *in vitro* activation of caspase-7.

[0047] Figure 5, Panel C depicts cytoplasmic extracts prepared from CHO and C.1 cells and incubated with (+) or without (-) 10 μ M cytochrome c and the various amounts of dATP (mM) as indicated.

[0048] Figure 6, Panel A depicts cell lysates from CHO and C.1 cells immunoprecipitated with anti-caspase-7 (lanes 1 and 2) or anti-caspase-3 (lanes 3 and 4) antibodies.

[0049] Figure 6, Panel B depicts cell lysates in extraction buffer from CHO and AD-1 cells were immunoprecipitated with anti-caspase-7 antibody (lanes 1 and 2). Whole cell extracts (WCE) from CHO and AD-1 cells were immunoblotted in parallel (lanes 3 and 4). The positions of GRP78, procaspase-7, and the deletion mutant form of GRP78 (Δ 78) are indicated.

[0050] Figure 6, Panel C depicts a schematic drawing of wild-type (WT) GRP78 and AD-1 showing the location of the signal sequence (S), the ATP-binding domain, and the AD-1 deletion spanning amino acids 175 to 201.

[0051] Figure 7, Panel A depicts a hydropathicity plot of GRP78 as generated using the Kyte-Doolittle method with a window size of 17. Four putative hydrophobic domains (I-IV) are identified. Represented below is a schematic drawing of the mature GRP78 protein with the hydrophobic domains IV and III as putative transmembrane domains generating carboxyl 35- and 50-kDa trypsin resistant fragments.

[0052] Figure 7, Panel B depicts limited trypsin digestion. Isolated microsomes from C.1 cells were either non-treated (lane 1) or subjected to trypsin digestion at the concentration of 0.01% (lane 2) or 0.05% (lane 2). At the end of the reaction, the amount of GRP78 was detected by Western blotting using the rabbit polyclonal anti-GRP78 antibody recognizing the carboxyl terminus (StressGen, Victoria, Canada) (left panel). The full-length GRP78 band is indicated by a closed arrow, and the 35- and 50-kDa proteolytic products are indicated by open arrows highlighted with a star. The same membrane was stripped and re-

probed with a rabbit polyclonal anti-calreticulin (CRT) antibody (middle panel) or a rabbit polyclonal anti-calnexin antibody recognizing the amino terminus of calnexin (right panel). The full-length CRT and calnexin are indicated by closed arrows, and the 70-kDa proteolytic product of calnexin is indicated by an open arrow highlighted by a star.

[0053] **Figure 7, Panel C** depicts sodium carbonate extraction. The microsome (M) fraction was either non-treated (lane 1) or treated with 100 mM sodium carbonate and separated into pellet (P) and supernatant (S) fractions (lanes 2 and 3, respectively). The protein samples from each fraction were separated by 10% SDS-PAGE and subjected to Western blotting with rabbit anti-GRP78 antibody (left panel), rabbit anti-calreticulin antibody (middle panel), and rabbit anti-calnexin antibody (right panel).

[0054] **Figure 8, Panel A** depicts cytoplasmic extracts (50 µg/lane) prepared from non-treated (Ctrl) and etoposide-treated (Etop) AD-1 and C.1 cells as separated on 10% SDS-PAGE and immunoblotted using anticaspase-7 antibody.

[0055] **Figure 8, Panel B** depicts the DNA fragmentation pattern of C.1 and AD-1 cells following etoposide treatment.

[0056] **Figure 8, Panel C** depicts cell death assays indicating that the ATP-binding domain of GRP78 is necessary for protection against etoposide-induced cell death. The S.D. is shown.

[0057] **Figure 9** depicts the relative cell cycle distribution of GRP-78. The percentage of cells in G1, G2, and S phase was determined.

[0058] **Figure 10** is a schematic showing the subcloning of the 320 bp grp78 exon 1 fragment.

[0059] **Figure 11A-C** shows the schemes used for subcloning. (A) shows the scheme for the subcloning of full-length His-tagged GRP78 into pShuttle CMV adenovirus; (B) shows the scheme for the subcloning of full-length His-Tagged GRP78 Full-length antisense (AS); and (C) shows the scheme used for the subcloning of GRP78 (320BP) antisense (AS) into PShuttle CMV adenovirus.

[0060] **Figure 12** shows the expression of His-tagged GRP78, GRP78(AS) and 320(AS) in adenovirus infected 293 T cells.

[0061] Figure 13A and B shows the results of transduced MDA-MB-435 cells treated with etoposide in the presence and absence of the 320(AS).

[0062] Figure 14 shows a Western blot of 293T cells. The concentrations of siRNA Grp78 II used were indicated on top.

[0063] Figure 15 shows a Western blot of MDA-MB-435 cells. The concentrations of siRNA Grp78 II used were indicated on top.

[0064] Figure 16 shows suppression of GRP78 by siRNA oligonucleotides results in enhanced sensitivity to etoposide-mediated cell death in breast cancer cells.

[0065] Figure 17A-B show the physical and functional interaction between GRP Blk. (A) 293T cells were either not treated (lanes 1, 2) or treated with 50 uM etoposide for 24 hours (lane 3). Cells were harvested and cells lysate immunoprecipitated with either goat IgG (lane 1) or goat anti-Blk antibody (lanes 2, 3). Western blots with anti-Blk antibody and anti-GRP78 antibody show co-immunoprecipitation of endogenous GRP78 with Blk. (B) 293T cells were transiently transfected with either pcDNA, CMV promoter driven expression vector for His-tagged GRP78, expression vector for Flag-tagged Glk-b5TM alone or in combination as indicated. After 48 hours, cell death was determined by trypan blue exclusion assay. The level of apoptosis observed in cells transfected with pcDNA3 was set as 1. The results showed overexpression of GRP78 protects 293T cells from death induced by transient transfection of ER-targeted Blk-b5TM.

DETAILED DESCRIPTION

[0066] Within the microenvironment of a solid tumor, unique stress conditions can lead to induction of GRPs. The data and invention described herein indicate that GRPs act as anti-apoptotic proteins. The GRP-mediated protection involves GRP interaction with effectors of apoptosis, leading to the blockage of cell death induced by drug treatment.

[0067] Thus, in accordance with the invention, GRPs (e.g., GRP74, GRP78 and GRP94) represent rational targets for chemotherapeutics, immunotherapeutics, antisense, ribozymes, siRNA and vaccines relevant to the treatment of cell proliferative diseases such as cancer. In view of their function

as molecular chaperones, the GRPs (e.g., GRP78 and 94) further represent rational targets for the development of therapeutics for tissue injury and stress, such as can occur in ischemic injuries including, but not limited to, organ (kidney, heart, lung, liver) transplantation, cerebral stroke, and myocardial infarct. Methods and compositions for modulating apoptosis are provided.

[0068] The invention provides methods and compositions useful to modulate apoptosis in a cell, tissue and/or subject.

"Apoptosis" refers to programmed cell death which occurs by an active, physiological process. Apoptosis plays an important role in developmental processes, including morphogenesis, maturation of the immune system, and tissue homeostasis whereby cell numbers are limited in tissues that are continually renewed by cell division. Apoptosis is an important cellular safeguard against tumorigenesis. An apoptotic cell or a cell going through "programmed cell death" exhibits one or more characteristics associated with timed or targeted cell death. Characteristics include inhibition of cell survival, growth, death or differentiation, protein/nucleic acid cleavage/fragmentation, chromatin condensation, membrane fragmentation, changes in expression or activity of one or more proteins that promote apoptosis or that inhibit apoptosis.

[0069] "Modulating" apoptosis means increasing, stimulating or inducing, or decreasing, inhibiting, blocking or preventing (e.g., prophylaxis) one or more characteristics of programmed cell death as described herein or known in the art. For example, the methods and compositions of the disclosure include agents (e.g., antisense molecules, ribozymes, polypeptides, small molecules, and the like) that increase, stimulate or induce apoptosis by inhibiting the activity or production of GRPs. The disclosure also includes agents and methods that increase the activity or production of GRPs to inhibit apoptosis in tissues or cells subject to damage due to ischemia and the like.

[0070] GRP78 binds transiently to nascent, secretory and transmembrane proteins and binds permanently to abnormally folded or processed proteins in the ER. GRP78 is thought to have a protective function during and after cellular stress when protein

processing in the ER is perturbed. GRP78 has been proposed as a possible target for several antitumor agents, principally radicicol and geldanamycin (Scheibel and Buckner, *Biochem Pharm* 56:675-82, 1998).

[0071] A potential yet heretofore uncharacterized protective role of GRP94 in ischemia is supported by the observation that expression of GRP94 is enhanced in hippocampus after transient forebrain ischemia of a duration known to result in neuronal death (Yagita et al., *J Neurochem* 72:1544-1551, 1999). GRP94 is similarly induced following acute kidney ischemia (Kuznetsov, *Proc Natl Acad Sci USA* 93:8584-8589, 1996). By comparison, heat-shock proteins, including HSP90, are over-expressed during the oxidative stress of reperfusion that generally follows ischemia. For example, the higher levels of GRP78 and GRP94 in the brains of immature rats when compared to those of adult animals account for the higher resistance of immature rats to seizure. In addition, specific induction of these GRPs in the dentate gyrus region of the adult rat brain following seizure is associated with a neuroprotective effect. For early-onset familial Alzheimer's disease (FAD), overexpression of GRP78 in neuroblastoma cells expressing a mutant presenilin-1 (PS1) protein was reported to restore resistance to ER stress.

[0072] Expression of GRP78 also prevents the aggregation and facilitates the proteasomal degradation of mutant prion proteins, which are implicated in neurodegenerative disorders such as prion diseases and transmissible spongiform encephalopathies. Induction of GRP78 has also been observed in endothelial cells damaged by reductive stress that was caused by hyperhomocysteinaemia, which, with both genetic and environmental components, is a common risk factor for thrombotic vascular events such as premature arteriosclerosis, stroke, myocardial infarction, and thrombosis. Therefore, the induction of GRP could be an adaptive response evolved in mammals to protect endothelial cells against stress-induced cell death.

[0073] Although apoptosis is mediated by diverse signals and complex interactions of cellular gene products, the results of these interactions ultimately feed into a cell death pathway that is evolutionarily conserved between humans and invertebrates.

The pathway, itself, is a cascade of proteolytic events analogous to that of the blood coagulation cascade.

[0074] Several gene families and products that are involved in the apoptotic pathway have been identified. Key to the apoptotic program is a family of cysteine proteases termed caspases. The human caspase family includes Ced-3, human ICE (interleukin-1 β converting enzyme) (caspase-1), ICH-1 (caspase-2), CPP32 (caspase-3), ICERelIII (caspase-4), ICERelIII (caspase-5), Mch2 (caspase-6), ICE-LAP3 (caspase-7), Mch5 (caspase-8), ICE-LAP6 (caspase-9), Mch4 (caspase-10), caspase 11-14 and others.

[0075] It has been demonstrated that caspases are required for apoptosis to occur. Moreover, caspases appear to be necessary for the accurate and limited proteolytic events that are the hallmark of classic apoptosis (see Salvesen and Dixit, *Cell* 91:443-446, 1997). During apoptosis, an initiator caspase zymogen is activated by autocatalytic cleavage, which then activates the effector caspases by cleaving their inactive zymogen (Salvesen and Dixit, *Proc. Natl. Acad. Sci. USA* 96:10964-10967, 1999; Srinivasula *et al.*, *Mol. Cell.* 1:949-957, 1998). The effectors are responsible for proteolytic cleavage of a number of cellular proteins leading to the characteristic morphological changes and DNA fragmentation that are often associated with apoptosis (reviewed in Cohen, *Biochem. J.* 326:1-16, 1997; Henkart, *Immunity* 4:195-201, 1996; Martin and Green, *Cell* 82:349-352, 1995; Nicholson and Thornberry, *TIBS* 257:299-306, 1997; Porter *et al.*, *BioEssays* 19:501-507, 1997; Salvesen and Dixit, *Cell* 91:443-446, 1997).

[0076] Among the executor caspases, caspase-7 has been reported to be associated with the ER. Upon induction of apoptosis, procaspase-7 (35 kDa) is first converted into a 32-kDa intermediate, which is further processed into active 20- and 11-kDa subunits. Western blotting data provided herein indicates that treating CHO cells with etoposide results in activation of caspase-7, giving rise to the 32-kDa intermediate form (Figure 5, Panel A). Upon longer exposure of the autoradiogram, the active 20- and 11-kDa forms were evident in the etoposide-treated cells. When GRP78 was overexpressed, a low level of caspase-7 activation

was detected in both the non-treated and etoposide-treated cells. These data indicate that GRP78 can suppress caspase-7 activation *in vivo* thereby inhibiting apoptosis. In addition, upon addition of cytochrome c, caspase-7 activation was higher in CHO cells than C.1 cells, as evidenced by the increase in the active 20- and 11-kDa forms in the CHO samples compared with the C.1 samples. In the presence of both cytochrome c and dATP, the suppressive effect of the C.1 samples was reversed. At 1 mM dATP, both cell lines showed equivalent amounts of the 32- and 20-kDa forms, indicating that dATP releases procaspase-7 from GRP78, resulting in its activation.

[0077] The invention demonstrates that over-expression in tissue culture systems of GRP78, GRP94 and adapt78 can protect cells against cell death. The invention also demonstrates that inhibitors of expression (e.g., antisense and RNAi) or inhibitors of GRP activity in tissue culture systems can induce apoptosis. Thus, the protective function of the GRPs is useful and beneficial in situations involving tissue or organ damage. This same protective function is detrimental in cancer by preventing apoptosis of cancer cells.

[0078] As demonstrated herein, GRP upregulation and/or overexpression is useful in limiting damage in organs exposed to stress. However, the anti-apoptotic function of GRPs also indicates that their induction in neoplastic cells and cell proliferative disorders could lead to cancer progression and drug resistance. In a variety of cancer cell lines, solid tumors and human cancer biopsies, the levels of GRP78 and GRP94 are elevated, correlating with malignancy. In addition, induction of GRP78 has been shown to protect cancer cells from immune surveillance, whereas suppressing the stress-mediated induction of GRP78 enhanced apoptosis, inhibited tumor growth and increased the cytotoxicity of chronic hypoxic cells.

[0079] Thus, the invention provides methods and compositions useful for targeted suppression of GRP expression or function in cancer cells as a novel approach to cancer therapy. For example, Genistein, which suppresses both the GRP and the heat shock responses, inhibits the growth of carcinogen-induced tumors in rats and in human leukemia cells transplanted into mice. In

another example, GRP94 has been shown to associate with and stabilize p185/erbB2 (also referred to HER-2/neu), which is commonly over-expressed in breast carcinomas and is associated with poor prognosis. Treatment of breast cancer cells with geldanamycin, an anti-proliferative agent, enables the degradation of p185 in the breast cancer cells by disrupting the GRP94-p185 complex.

[0080] Pre-induction of GRP in a variety of human cancer cell lines confers resistance to inhibitors of topoisomerase II (e.g., etoposide) but increases sensitivity to DNA cross-linking agents such as cisplatin. Direct suppression of GRP94 levels by antisense knockdown strategies results in enhanced sensitivity to etoposide-induced cell death.

[0081] Accordingly, the invention provides methods and compositions useful in reducing the anti-apoptotic effect of GRPs, increase sensitivity of cancer cells to chemotherapeutic agents, and promote apoptosis of neoplastic cells. The methods and compositions of the invention inhibit the production or activity of GRPs in neoplastic cells (e.g., cancer cells) and tissues.

[0082] As will be discussed below, the invention provides the first evidence that a population of GRPs is integrally-associated with the membrane of the endoplasmic reticulum. These GRPs interact with a cytosolic component to mediate apoptosis. A "cytosolic component that mediates apoptosis", as used herein, is any polypeptide, or group of polypeptides that cooperate in the initiation or facilitation of apoptosis. For example, the interaction between GRP78 and caspase-7 and/or the interaction between GRP94 and p185/erbB2 is involved in GRPs ability to modulate apoptosis. The interaction can be, for example, with caspase-7 individually, or as part of a group of other polypeptides involved in the apoptosis pathway.

[0083] The invention further provides the first evidence that complex formation between endogenous GRP78 and caspase-7 occurs in association with the endoplasmic reticulum. While the data provided herein indicates that GRP78 and caspase-7 interact, the invention is not limited to a direct interaction between the two proteins. It is understood that the invention encompasses a

cytosolic component that is a complex of polypeptides, including caspase-7, or caspase-7 individually. By preventing the interaction of GRP78 with caspase-7, the agent modulates apoptosis by promoting apoptosis. Alternatively, by promoting the interaction of GRP78 with caspase-7, an agent would modulate apoptosis by inhibiting apoptosis.

[0084] In one embodiment, the invention provides a method of modulating apoptosis by contacting a GRP (e.g., GRP74, 78, and/or 94) with an agent that regulates the interaction of the GRP protein with a cytosolic component that mediates apoptosis. As used herein, the term "interact" includes any detectable interactions between molecules. The term "interact" is also meant to include "binding" interactions between molecules. Interactions can, for example, be protein-protein, protein-nucleic acid, and nucleic acid-nucleic acid in nature including hydrogen-bond interactions, covalent-bond interactions and the like.

[0085] An "agent", as used herein, can be any molecule including, for example, a polypeptide, an antibody, a nucleic acid (e.g., an antisense, ribozyme, siRNA or the like) or a small molecule. An agent can be a "therapeutic agent" useful for treating disorders associated with cell proliferation including anti-neoplastic agents and anti-inflammatory agents.

[0086] The invention provides apoptotic agents (e.g., GRP antagonists) comprising agents that inhibit the anti-apoptotic affect of GRPs (e.g., GRP78). In one aspect of the invention, a small molecule such as dATP is used to prevent the interaction, and/or disrupt the interaction of GRP78 with caspase-7 thereby inhibiting the anti-apoptotic activity of GRP78. In another aspect, agents are provided that inhibit transcription from a GRP (e.g., GRP78) gene. For example, versielostatin (VST) is useful to inhibit transcription from GRP78 (Park et al., J. Nat. Canc. Inst., 96(17):1300-1310, 2004; the disclosure of which is incorporated herein by reference). In another aspect, inhibitory nucleic acid molecules (e.g., antisense, ribozymes, siRNA) molecules are used to inhibit the production of GRPs (e.g., GRP78). In one aspect, the apoptotic agents provide a method for inducing apoptosis by inhibiting the production of GRP78 thereby

inhibiting the anti-apoptotic affect of GRP78 in a cell. The apoptotic agents of the invention are useful in treating neoplastic and cancer disorders by promoting apoptosis in cells expressing GRPs such as GRP78.

[0087] In embodiments where apoptosis is desired, the agent that directly reduces expression/activity of GRP can be a nucleic acid that reduces expression of GRP. In embodiments where anti-apoptotic activity is desired, the nucleic acid can be a sense nucleic acid that encodes a GRP protein (e.g., introduction into a cell can increase the cells GRP activity).

[0088] In one embodiment where apoptotic activity is desired an apoptotic agent such as a GRP antagonist is used. In one aspect, an apoptotic nucleic acid agent is used. An apoptotic nucleic acid agent can be an antisense nucleic acid that hybridizes to mRNA encoding a GRP. Antisense nucleic acid molecules for use with the invention are those that specifically hybridize under cellular conditions to cellular mRNA and/or genomic DNA encoding a GRP protein in a manner that inhibits expression of the GRP protein, e.g., by inhibiting transcription and/or translation. The binding may be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interactions in the major groove of the double helix.

[0089] Antisense constructs can be delivered as an expression plasmid which, when transcribed in the cell, produces RNA which is complementary to at least a unique portion of the mRNA and/or endogenous gene which encodes a GRP protein. Alternatively, the antisense construct can take the form of an oligonucleotide probe generated ex vivo which, when introduced into a GRP protein expressing cell, causes inhibition of GRP protein expression by hybridizing with an mRNA and/or genomic DNA coding for a GRP protein. Such antisense molecules may comprise modified nucleotides that are resistant to endogenous nucleases, e.g., exonucleases and/or endonucleases, and are therefore stable in vivo. Additionally, general approaches to constructing oligomers useful in antisense therapy have been reviewed, for example, by Van der Krol et al., *Biotechniques* 6:958-976, 1988; and Stein et al., *Cancer Res.* 48:2659-2668, 1988.

[0090] Antisense approaches involve the design of nucleic acid molecules (e.g., DNA, RNA, or modified forms thereof) that are complementary to nucleic acids encoding a GRP. The antisense molecules will bind to GRP mRNA transcripts and prevent translation or to the endogenous gene and prevent transcription. Absolute complementarity is not required. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

[0091] Antisense nucleic acid molecules that are complementary to the 5' end of an mRNA, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should work most efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated region of mRNAs have been shown to be effective at inhibiting translation of mRNAs as well. (Wagner, R., Nature 372:333, 1994). Therefore, antisense molecules complementary to either the 5' or 3' untranslated, non-coding regions of a GRP mRNA or gene may be used in an antisense approach to inhibit transcription and/or translation of endogenous GRP gene or mRNA, respectively. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon.

[0092] The coding strand sequences of GRPs are known. For example, Table 1 provides the coding sequences of some GRPs and related molecular chaperones. Other sequence will be readily apparent and available through GenBank.

Table 1

GRP	GenBank/NCBI Accession No.
GRP58	NM_005313 (SEQ ID NO:5 and 6)
GRP78	BC020235 and P11021 (SEQ ID NO:1 and 2)
GRP94	BC066656 and AAH66656 (SEQ ID NO:15 and 16)
Calreticulin (CALR)	NM_004343 and BT007448 (SEQ ID NO:7 and 8)
calreticulin 3 (CALR3)	NM_145046 (SEQ ID NO:9 and 10)
PDI	E03087 and NM_006849 (pancreatic) (SEQ ID NO:11 and 12)
ERP72	HUMERP72H (SEQ ID NO:13 and 14)

Each of the accession numbers and their content is incorporated herein by reference. Given the coding strand sequences encoding, for example, GRP78, antisense nucleic acids can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a GRP polynucleotide (e.g., GRP78 mRNA), or can be an oligonucleotide, which is antisense to only a portion of the coding or noncoding region of a GRP. For example, the antisense oligonucleotide can be complementary to the region surrounding the transcriptional or translation start site of GRP mRNA. An antisense oligonucleotide can be, for example, about 10, 20, 25, 50, 100, 150, 200, 250, 300, 350, 400 or more nucleotides in length. An antisense nucleic acid molecule can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. Antisense nucleic acid molecules of the invention may be synthesized by standard methods known in the art, e.g. by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al., Nucl. Acids Res. 16:3209, 1988; or methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451, 1988). An antisense nucleic acid molecule can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids.

[0093] The invention includes antisense nucleic acid molecules, which hybridize with a polynucleotide sequence comprising a sequence encoding a GRP. The antisense molecules employed may be unmodified or modified RNA or DNA molecules. Suitable modifications include, but are not limited to, the ethyl or methyl phosphonate modification disclosed in U.S. Pat. No. 4,469,863, the disclosure of which is incorporated by reference, and the phosphorothioate modifications to deoxynucleotides described by LaPlanche, et al., 1986 Nucleic Acids Research, 14:9081, and by Stec, et al., 1984 J. Am. Chem Soc. 106:6077. The

modification to the antisense oligonucleotides is typically a terminal modification in the 5' or 3' region. Alternatively, the antisense molecules can have chimeric backbones of two or more modified nucleic acid bases, which are modified by different methods. Such methods include, for example, amino acid or nucleic acid modification as described by K. Ramasamy and W. Seifert (Bioorganic and Medicinal Chemistry Letters, 6(15):1799-1804 (1996)) or 4' sugar substituted oligonucleotides described by G. Wang and W. Seifert (Tetrahedron Letters, 37(36):6515-6518 (1996)).

[0094] Phosphodiester-linked oligonucleotides are particularly susceptible to the action of nucleases in serum or inside cells, and therefore in a one embodiment the antisense nucleic acid molecules of the invention are phosphorothioate or methyl phosphonate-linked analogues, which have been shown to be nuclease-resistant. Specific examples of some antisense oligonucleotides envisioned for this invention may contain phosphorothioates, phosphotriesters, methyl phosphonates, short chain alkyl or cycloalkyl intersugar linkages or short chain heteroatomic or heterocyclic intersugar ("backbone") linkages. Typical are phosphorothioates and those with $\text{CH}_2\text{NHOCH}_2$, $\text{CH}_2\text{N}(\text{CH}_3)\text{OCH}_2$, $\text{CH}_2\text{ON}(\text{CH}_3)\text{CH}_2$, $\text{CH}_2\text{N}(\text{CH}_3)\text{N}(\text{CH}_3)\text{CH}_2$ and $\text{ON}(\text{CH}_3)\text{CH}_2\text{CH}_2$ backbones (where phosphodiester is OPOCH_2). Also typical are oligonucleotides having morpholino backbone structures (Summerton and Weller, U.S. Pat. No. 5,034,506). In other embodiments, 2'-methylribonucleotides (Inoue, et al., Nucleic Acids Research, 15:6131, 1987) and chimeric oligonucleotides that are composite RNA-DNA analogues (Inoue, et al., FEBS Lett., 215:327, 1987) may also be used for the purposes described herein. Finally, DNA analogues, such as peptide nucleic acids (PNA) are also included (Egholm, et al., Nature 365:566, 1993; Nielsen et al., Science, 254:1497, 1991) can be used according to the invention. Other oligonucleotides may contain alkyl and halogen-substituted sugar moieties comprising one of the following at the 2' position: OH, SH, SCH_3 , F, OCN, OCH_3OCH_3 , $\text{OCH}_3\text{O}(\text{CH}_2)_n\text{CH}_3$, $\text{O}(\text{CH}_2)_n\text{NH}_2$ or $\text{O}(\text{CH}_2)_n\text{CH}_3$ where n is from 1 to about 10; C_1 to C_{10} lower alkyl, substituted lower alkyl, alkaryl or aralkyl; Cl; Br; CN; CF_3 ; OCF_3 ; O, S, or N-alkyl; O, S or N alkenyl; SOCH_3 ; SO_2CH_3 ; ONO_2 ; NO_2 ; N_3 ; NH_2 ;

heterocycloalkyl; heterocycloalkaryl; aminoalkylamino; polyalkylamino; substituted silyl; an RNA cleaving group; a cholesteryl group; a conjugate; a reporter group; an intercalator; a group for improving the pharmacokinetic properties of a oligonucleotide; or a group for improving the pharmacodynamic properties of a oligonucleotide and other substituents having similar properties. Oligonucleotides may also have sugar mimetics such as cyclobutyls in place of the pentofuranosyl group. Other embodiments may include at least one modified base form or "universal base" such as inosine. The preparation of base-modified nucleosides, and the synthesis of modified oligonucleotides using said base-modified nucleosides as precursors, has been described, for example, in U.S. Pat. Nos. 4,948,882 and 5,093,232. These base-modified nucleosides have been designed so that they can be incorporated by chemical synthesis into either terminal or internal positions of a oligonucleotide. Such base-modified nucleosides, present at either terminal or internal positions of a oligonucleotide, can serve as sites for attachment of a peptide or other antigen. Nucleosides modified in their sugar moiety have also been described (e.g., U.S. Pat. No. 5,118,802 and U.S. Pat. No. 5,681,940, both of which are incorporated by reference) and can be used similarly. Persons of ordinary skill in this art will be able to select other linkages for use in the invention. These modifications also may be designed to improve the cellular uptake and stability of the oligonucleotides. It is understood that depending on the route or form of administration of the antisense oligonucleotides of the invention, the modification or site of modification will vary (e.g., 5' or 3' modification). One of skill in the art can readily determine the appropriate modification without undue experimentation.

[0095] Examples of modified nucleotides which can be used to generate the antisense molecules include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-

methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

Alternatively, the antisense molecule can be produced biologically using an expression vector into which a GRP polynucleotide or fragment thereof has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest).

[0096] In a specific embodiment, the antisense molecule comprises a sequence as set forth in SEQ ID NO:3 or a fragment thereof. Thus, in one aspect, the antisense molecule includes (i) SEQ ID NO:3; (ii) fragments of SEQ ID NO:3 which inhibit the production of GRP78; (iii) SEQ ID NO:3 or a fragment thereof wherein T is replaced with U; (iv) SEQ ID NO:3 having a modified backbone; and (v) any of (i) - (iv) capable of interacting with a polynucleotide encoding GRP78. Other specific antisense molecules include antisense fragments of nucleic acids encoding GRPs (e.g., fragments of SEQ ID NO:3, antisense fragments of GRP94 and the like; see Table 1).

[0097] Small double stranded nucleic acid molecules that can silence a GRP are also provided as part of the invention. Small interfering RNA (siRNA) molecules are provided that interfere with RNA transcription. RNA interference (RNAi) is a mechanism of post-transcriptional gene silencing in which double-stranded RNA (dsRNA) corresponding to a gene (or coding region) of interest is introduced into a cell or an organism, resulting in degradation of the corresponding mRNA. The RNAi effect persists for multiple cell divisions before gene expression is regained. RNAi is therefore an extremely powerful method for making

targeted knockouts or "knockdowns" at the RNA level. RNAi has proven successful in human cells, including human embryonic kidney and HeLa cells (see, e.g., Elbashir et al., *Nature*, 411(6836):494-8, 2001). In one embodiment, GRP (e.g., GPR78) silencing can be induced in mammalian cells by enforcing endogenous expression of RNA hairpins (see Paddison et al., *PNAS USA* 99:1443-1448, 2002). In another embodiment, transfection of small (21-23 nt) dsRNA specifically inhibits gene expression (reviewed in Caplen, *Trends in Biotechnology* 20:49-51, 2002).

[0098] Briefly, dsRNA corresponding to a portion of a GRP gene to be silenced is introduced into a cell. The dsRNA can be longer sequences that are subsequently digested into 21-23 nucleotide siRNAs, or short interfering RNAs, or the 21-23 nucleotide siRNA molecules may be directly provided to the cell. The siRNA duplexes bind to a nuclease complex to form what is known as the RNA-induced silencing complex, or RISC. The RISC targets the homologous transcript by base pairing interactions between one of the siRNA strands and the endogenous mRNA. It then cleaves the mRNA about 12 nucleotides from the 3' terminus of the siRNA (reviewed in Sharp et al., *Genes Dev* 15: 485-490, 2001; and Hammond et al., *Nature Rev Gen* 2: 110-119, 2001).

[0099] RNAi technology in gene silencing utilizes standard molecular biology methods. dsRNA corresponding to the sequence from a target gene to be inactivated can be produced by standard methods, e.g., by simultaneous transcription of both strands of a template DNA (corresponding to the target sequence) with T7 RNA polymerase. Kits for production of dsRNA for use in RNAi are available commercially, e.g., from New England Biolabs, Inc. Methods of transfection of dsRNA or plasmids engineered to make dsRNA are routine in the art.

[00100] Gene silencing effects similar to those of RNAi have been reported in mammalian cells with transfection of a mRNA-cDNA hybrid construct (Lin et al., *Biochem Biophys Res Commun*, 281(3):639-44, 2001), providing yet another strategy for gene silencing.

[00101] Accordingly, the invention provides small interfering nucleic acids (siNA) that interact with a polynucleotide encoding a GRP. In one aspect, the invention provides siNA comprising (i)

a sequence as set forth in SEQ ID NO:1, 5, 7, 9, 11, 13, or 15 as set forth in Table 1, and their complement that is 21-23 nucleotides in length and comprises an AA dinucleotide at the 5' end and a GC content of 30-50%; (ii) a double stranded nucleic acid comprising 5'-AAGGTTACCCATGCAGTTGTT-3' (SEQ ID NO:4) and its complement; (iii) a sequence as set forth in SEQ ID NO:4 and its complement wherein T is replaced with U; and any of (i) - (iii) wherein the siNA has a modified backbone as described above.

[00102] Ribozyme molecules designed to catalytically cleave GRP mRNA transcripts can also be used to prevent translation of GRP mRNA and expression of GRP protein (see, e.g., PCT Publication No. WO 90/11364, published Oct. 4, 1990; Sarver et al., Science 247:1222-1225, 1990 and U.S. Pat. No. 5,093,246). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy GRP mRNAs, the use of hammerhead ribozymes is typical. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, Nature 334:585-591, 1988. Typically the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of GRP mRNA; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts. Ribozymes within the invention can be delivered to a cell using a vector.

[00103] Endogenous GRP gene expression can also be reduced by inactivating or "knocking out" the GRP gene or its promoter using targeted homologous recombination. See, e.g., Kempin et al., Nature 389: 802 (1997); Smithies et al., Nature 317:230-234, 1985; Thomas and Capecchi, Cell 51:503-512, 1987; and Thompson et al., Cell 5:313-321, 1989. For example, a mutant, non-functional GRP gene variant (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous GRP gene (either the coding regions or regulatory regions of the GRP gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express GRP protein *in vivo*.

[00104] The nucleic acids, ribozyme, RNAi, and triple helix molecules used in the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the nucleic acid molecule. Such DNA sequences may be incorporated into a wide variety of vectors, which incorporate suitable RNA polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

[00105] In yet another aspect, the invention provides polypeptide antagonists of GRP activity. Such polypeptides include antibodies, soluble domains of a GRP and polypeptides that interact with a transmembrane domain of a GRP to prevent incorporation of the GRP into a membrane of a cell. For example, as described herein, GRP78 comprises a cytosolic domain and transmembrane domains. The cytosolic domain (e.g., a soluble domain) interacts with cytosolic proteins that induce apoptosis. By inhibiting the interaction of the GRP with the cytosolic proteins that induce apoptosis, the anti-apoptotic effect of the GRP can be inhibited. Furthermore, GRPs (e.g., GRP78 comprises hydrophobic transmembrane domain(s)). For example, hydrophobic transmembrane domain III (amino acids 210-260 of SEQ ID NO:2) and/or domain IV (amino acids 400-450 of SEQ ID NO:2) of the protein of GRP78 are useful targets. Polypeptide agents that regulate the ability of a GRP polypeptide to integrate in to the membrane are candidates for modulating apoptosis. For example, a polypeptide agent that inhibits the ability of GRP78 to integrate into the membrane will also be capable of promoting apoptosis because it will prevent GRP78 from interacting with cytosolic components that are required to promote apoptosis. Thus, variants and fragments of a GRP protein (e.g., fragments, analogs and derivatives of native GRP proteins) may also be used in methods

of the invention to inhibit anti-apoptotic activity of a GRP (e.g., a GRP antagonist).

[00106] As discussed above, the topology of GRP78 indicates that part of GRP78 is exposed to the cytosol, allowing it to interact with cytosolic components. Thus, in another embodiment, the invention provides a method of modulating apoptosis by contacting GRP78 with an agent that inhibits or prevents the ability of the protein to integrate in to the membrane of the endoplasmic reticulum. In yet another embodiment, the invention provides a method of identifying an agent that modulates the interaction of GRP78 with a membrane by providing a polypeptide that includes hydrophobic transmembrane domain III (amino acids 210-260 of SEQ ID NO:2) and/or domain IV (amino acids 400-450 of SEQ ID NO:2) of the protein of GRP78. The polypeptide can be contacted with an agent, and the effect of the agent on the interaction can be determined. Agents that regulate the ability of the polypeptide to integrate in to the membrane are candidates for modulating apoptosis. For example, an agent that inhibits the ability of GRP78 to integrate in to the membrane will also be capable of promoting apoptosis because it will prevent GRP78 from interacting with cytosolic components that are required to promote apoptosis. Accordingly, a method of the invention includes modulating apoptosis by regulating the interaction between ER membrane bound (i.e., integrally associated) GRP78 and a cytosolic component that mediates apoptosis, such as, for example, a complex of proteins that includes caspase-7.

[00107] In a further embodiment, the invention provides a method of identifying an agent that modulates the interaction of GRP78 with a cytosolic component that mediates apoptosis. The method includes providing GRP78 integrally-associated with a membrane, providing a cytosolic component comprising at least one caspase, providing an agent, contacting the protein with the component and the agent, simultaneously or in succession, and determining the effect of the agent on the interaction of the protein and the component as compared to a control.

[00108] The invention provides methods and compositions that are useful to promote apoptosis in a tissue or cell comprising contacting the tissue or cell with an agent that inhibits the

anti-apoptotic activity of a GRP (e.g., GRP78). The methods and compositions are useful in treating neoplastic disorders including cancer and tumor growth. The methods and compositions can be used alone or in combination with other neoplastic/cancer therapies. For example, the methods and compositions of the invention can be used in combination with chemotherapeutic drugs such as, but not limited to, 5-fluorouracil (5FU), cytosine arabinoside, cyclophosphamide, cisplatin, carboplatin, doxyrubicin, etoposide, taxol, and alkylating agents. Furthermore, combinations of nucleic acid inhibitors may be used (e.g., a combination of SEQ ID NO:3 and SEQ ID NO:4).

[00109] In another aspect, variants and fragments of a GRP protein (e.g., fragments, analogs and derivatives of native GRP proteins) may also be used in methods of the invention. Such variants include, e.g., a polypeptide encoded by a naturally occurring allelic variant of a native GRP polynucleotide, a polypeptide encoded by an alternative splice form of a native GRP polynucleotide, a polypeptide encoded by a homolog of a native GRP polynucleotide, and a polypeptide encoded by a non-naturally occurring variant of a native GRP polynucleotide.

[00110] GRP protein variants have a polypeptide sequence that differs from a native GRP protein in one or more amino acids. The peptide sequence of such variants can feature a deletion, addition, or substitution of one or more amino acids of a native GRP polypeptide. Amino acid insertions are typically of about 1 to 4 contiguous amino acids, and deletions are preferably of about 1 to 10 contiguous amino acids. In some applications, variant GRP proteins substantially maintain a native GRP protein functional activity (e.g., ability to mediate anti-apoptotic activity, bind caspase-7 and the like; are agonists). Such functional variants are useful in treating disorders associated with apoptosis, e.g., ischemia and the like, where it is desirable to reduce apoptosis. For other applications, variant GRP proteins lack or feature a significant reduction in a GRP protein functional activity. Where it is desired to retain a functional activity of native GRP protein, a GRP protein variant can be made by expressing nucleic acid molecules that feature silent or conservative changes. Variant GRP proteins with

substantial changes in functional activity can be made by expressing nucleic acid molecules that feature less than conservative changes.

[00111] GRP protein fragments corresponding to one or more particular motifs and/or domains or to arbitrary sizes, for example, at least 5, 10, 25, 50, 75, 100, 125, 150, or 175 amino acids in length may be utilized in methods of the invention. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional solid phase f-Moc or t-Boc chemistry. For example, a GRP protein used in the methods of the invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or divided into overlapping fragments of a desired length. The fragments can be produced (recombinantly or by chemical synthesis) and tested to identify those fragments, which can function as either agonists or antagonists of a native GRP protein.

[00112] Methods of the invention may also involve recombinant forms of the GRP proteins. Recombinant polypeptides, in addition to native GRP protein, are encoded by a nucleic acid that has at least 85% sequence identity (e.g., 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100%) with a native GRP nucleic acid sequence. In a one embodiment, variant GRP proteins lack one or more functional activities of a native GRP protein.

[00113] GRP protein variants can be generated through various techniques known in the art. For example, GRP protein variants can be made by mutagenesis, such as by introducing discrete point mutation(s), or by truncation. Mutation can give rise to a GRP protein variant having substantially the same, or merely a subset of the functional activity of a native GRP protein.

Alternatively, antagonistic forms of the protein can be generated which are able to inhibit the function of the naturally occurring form of the protein, such as by competitively binding to another molecule that interacts with GRP protein (e.g., interferes with the interaction of GRP78 and caspase-7). In addition, agonistic forms of the protein may be generated that constitutively express one or more GRP functional activities. Other variants of GRP proteins that can be generated include those that are resistant

to proteolytic cleavage, as for example, due to mutations that alter protease target sequences. Whether a change in the amino acid sequence of a peptide results in a GRP protein variant having one or more functional activities of a native GRP protein can be readily determined by testing the variant for a native GRP protein functional activity.

[00114] Nucleic acid molecules encoding GRP fusion proteins may be used in methods of the invention. Such nucleic acids can be made by preparing a construct (e.g., an expression vector) that expresses a GRP fusion protein when introduced into a suitable host. For example, such a construct can be made by ligating a first polynucleotide encoding a GRP protein fused in frame with a second polynucleotide encoding another protein such that expression of the construct in a suitable expression system yields a fusion protein.

[00115] As another example, GRP protein variants can be generated from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate polynucleotide sequence can be carried out in an automatic DNA synthesizer, and the synthetic polynucleotide then ligated into an appropriate expression vector. The purpose of a degenerate set of polynucleotides is to provide, in one mixture, all of the sequences encoding the desired set of potential GRP protein sequences. The synthesis of degenerate oligonucleotides is well known in the art (see for example, Narang, Tetrahedron 39:3, 1983; Itakura et al., Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules, ed. A G Walton, Amsterdam: Elsevier pp 273-289, 1981; Itakura et al., Annu. Rev. Biochem. 53:323, 1984; Itakura et al., Science 198:1056, 1984; Ike et al., Nucleic Acid Res. 11:477, 1983. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al., Science 249:386-390, 1990; Roberts et al., Proc. Natl. Acad. Sci. USA 89:2429-2433, 1992; Devlin et al., Science 249: 404-406, 1990; Cwirla et al., Proc. Natl. Acad. Sci. USA 87: 6378-6382, 1990; as well as U.S. Pat. Nos. 5,223,409; 5,198,346; and 5,096,815).

[00116] Similarly, a library of coding sequence fragments can be provided for a GRP clone in order to generate a variegated population of GRP polypeptide fragments for screening and

subsequent selection of fragments having one or more GRP agonist (e.g., anti-apoptotic) or antagonist (e.g., apoptotic) activities. A variety of techniques are known in the art for generating such libraries, including chemical synthesis. In one embodiment, a library of coding sequence fragments can be generated by (i) treating a double-stranded PCR fragment of a GRP polynucleotide coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule; (ii) denaturing the double-stranded DNA; (iii) renaturing the DNA to form double-stranded DNA which can include sense/antisense pairs from different nicked products; (iv) removing single-stranded portions from reformed duplexes by treatment with S1 nuclease; and (v) ligating the resulting fragment library into an expression vector. By this exemplary method, an expression library can be derived which codes for N-terminal, C-terminal and internal fragments of various sizes.

[00117] A wide range of techniques are known in the art for screening products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for products having a certain property. Such techniques will be generally adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of GRP polynucleotide variants. The most widely used techniques for screening large libraries typically involve cloning the library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates relatively easy isolation of the vector encoding the gene whose product was detected. One screening technique useful to measure anti-apoptotic and apoptotic effects includes determining cell survival in the presence of etoposide. Recombinant products that inhibit (e.g., are antagonistic of) native GRP function will show an increase in cell-death in the presence of etoposide, whereas products that promote (e.g., are agonists of) GRP function will show a reduced cell-death compared to controls. Thus, the invention provides methods of mutagenizing and screening gene products to determine their agonistic and/or antagonistic effect on GRP activity. Agents

having agonistic effects are useful for treating ischemia and related disorders that cause unwanted cell death. Agents that have antagonistic effects are useful to treat diseases and disorders having unwanted cell growth (e.g., cell proliferative disorders associated with cancer and the like).

[00118] Methods of the invention may utilize mimetics, e.g. peptide or non-peptide agents, that are able to disrupt binding of a GRP protein to other proteins or molecules with which a native GRP protein interacts (e.g., caspase-7). Thus, the mutagenic techniques described herein can also be used to map which determinants of GRP protein participate in the intermolecular interactions involved in, for example, binding of a GRP protein to other proteins which function to carry out apoptosis. Although the invention described thus far has focused on methods and compositions useful to promote apoptosis by inhibiting anti-apoptotic GRPs, the invention also includes methods and compositions that promote anti-apoptotic activity (e.g., in response ischemic injury and the like).

[00119] The invention also provides methods and compositions, which promote anti-apoptotic activity of GRPs (e.g., GRP78 and 94). The compositions and methods of this aspect of the invention are useful to treat tissue damage or potential damage to cells or tissues resulting from, for example, stroke, heart attack, hypoxia, hypoglycemia, brain or spinal cord ischemia, or brain or spinal cord trauma. The methods use agents (including, e.g., small molecules, polypeptides, peptides, and nucleic acids) that promote GRP activity, GRP expression, GRP production, and/or GRP association with polypeptides resulting in an inhibition of apoptosis.

[00120] The invention provides methods and compositions for modulating GRP expression and/or activity in a cell. Numerous agents for modulating expression/activity of intracellular proteins such as GRP in a cell are known. Any of these suitable for the particular system being used may be employed. Typical agents for promoting (e.g., agonistic) activity of GRPs include mutant/variant GRP polypeptides or fragments, nucleic acids encoding a functional GRP polypeptide or variant, and small organic or inorganic molecules.

[00121] Examples of proteins that can modulate GRP expression and/or activity in a cell include native GRP proteins (e.g., to upregulate activity) or variants thereof that can compete with a native GRP protein for binding ligands such as a caspase (e.g., to downregulate apoptosis). Such protein variants can be generated through various techniques known in the art as described herein. For example, GRP protein variants can be made by mutagenesis, such as by introducing discrete point mutation(s), or by truncation (e.g., of the transmembrane region). Mutation can give rise to a GRP variant or fragment having substantially the same, improved, or merely a subset of the functional activity of a native GRP protein. Agonistic (or superagonistic) forms of the protein may be generated that constitutively express one or more GRP functional activities. Other variants of GRP polypeptides that can be generated include those that are resistant to proteolytic cleavage, as for example, due to mutations which alter protease target sequences. Whether a change in the amino acid sequence of a peptide results in a GRP protein variant having one or more functional activities of a native GRP protein can be readily determined by testing the variant for a native GRP protein functional activity (e.g., modulating apoptosis).

[00122] As previously noted, the invention provides a method of inhibiting apoptosis in a tissue by overexpressing GRP78 and/or GRP94 in the targeted tissue. Overexpression of a polypeptide in a target tissue can be accomplished by any method known to the skilled artisan. For example, a nucleic acid sequence encoding GRP78 and/or GRP94 can be incorporated in a nucleic acid construct suitable for expression in a targeted tissue. Generally, the construct will possess the appropriate regulatory sequences for expression in the targeted tissue.

[00123] The invention provides methods involving modulating levels of GRP in a cell. The cell may be *in vitro* or *in vivo*. Where the cell is *in vivo* it may be present in an animal subject such as any mammal including humans, rats, mice, cats, dogs, goats, sheep, horses, monkeys, apes, rabbits, cattle, and the like. The animal subject can be in any stage of development including adults, young animals, and neonates. Animal subjects

also include those in a fetal stage of development. Target tissues can be any within the animal subject such as liver, kidney, heart (e.g., cardiomyocytes), lungs, components of gastrointestinal tract, pancreas, gall bladder, urinary bladder, skeletal muscle, the central nervous system including the brain, eye, skin, bones, and the like.

[00124] Various techniques using viral vectors for the introduction of a GRP nucleic acid (e.g., an inhibitory nucleic acid such as an antisense molecule or a GRP variant) into a cell may be utilized in the methods of the invention. Viral vectors for use in the invention are those that exhibit low toxicity to a host cell and induce production of therapeutically useful quantities of a GRP protein or antisense and/or RNAi nucleic acids in a tissue-specific manner. Viral vector methods and protocols that may be used in the invention are reviewed in Kay et al. *Nature Medicine* 7:33-40, 2001. The use of specific vectors, including those based on adenoviruses, adeno-associated viruses, herpes viruses, and retroviruses are described in more detail below.

[00125] The use of recombinant adenoviruses as gene therapy vectors is discussed in W. C. Russell, *Journal of General Virology* 81:2573-2604, 2000; and Bramson et al., *Curr. Opin. Biotechnol.* 6:590-595, 1995. Adenovirus vectors are useful in the invention because they (1) are capable of highly efficient gene expression in target cells and (2) can accommodate a relatively large amount of heterologous (non-viral) DNA. A typical form of recombinant adenovirus is a "helper-dependent" adenovirus vector. Such a vector features, for example, (1) the deletion of all or most viral-coding sequences (those sequences encoding viral proteins), (2) the viral inverted terminal repeats (ITRs) which are sequences required for viral DNA replication, (3) up to 28-32 kb of "exogenous" or "heterologous" sequences (e.g., sequences encoding a GRP protein, a GRP variant, an antisense molecule, or an RNAi molecule), and (4) the viral DNA packaging sequence which is required for packaging of the viral genomes into infectious capsids

[00126] Other viral vectors that might be used in the invention are adeno-associated virus (AAV)-based vectors. AAV-

based vectors are advantageous because they exhibit high transduction efficiency of target cells and can integrate into the host genome in a site-specific manner. Use of recombinant AAV vectors is discussed in detail in Tal, J., J. Biomed. Sci. 7:279-291, 2000 and Monahan and Samulski, Gene Therapy 7:24-30, 2000. A typical AAV vector comprises a pair of AAV inverted terminal repeats (ITRs) which flank at least one cassette containing a tissue (e.g., heart)- or cell (e.g., cardiomyocyte)-specific promoter operably linked to a GRP nucleic acid. The DNA sequence of the AAV vector, including the ITRs, the promoter and GRP gene may be integrated into the host genome.

[00127] The use of herpes simplex virus (HSV)-based vectors is discussed in detail in Cotter and Robertson, Curr. Opin. Mol. Ther. 1:633-644, 1999. HSV vectors deleted of one or more immediate early genes (IE) are advantageous because they are generally non-cytotoxic, persist in a state similar to latency in the host cell, and afford efficient host cell transduction. Recombinant HSV vectors can incorporate approximately 30 kb of heterologous nucleic acid. A typical HSV vector is one that: (1) is engineered from HSV type I, (2) has its IE genes deleted, and (3) contains a tissue-specific promoter operably linked to a GRP nucleic acid (e.g., an antisense, RNAi, GRP variant). HSV amplicon vectors may also be useful in various methods of the invention. Typically, HSV amplicon vectors are approximately 15 kb in length, and possess a viral origin of replication and packaging sequences.

[00128] Retroviruses such as C-type retroviruses and lentiviruses are also useful in the invention. For example, retroviral vectors may be based on murine leukemia virus (MLV). See, e.g., Hu and Pathak, Pharmacol. Rev. 52:493-511, 2000 and Fong et al., Crit. Rev. Ther. Drug Carrier Syst. 17:1-60, 2000. MLV-based vectors may contain up to 8 kb of heterologous nucleic acids in place of the viral genes. The heterologous nucleic acids typically comprise a tissue-specific promoter and a GRP nucleic acid.

[00129] Additional retroviral vectors that might be used are replication-defective lentivirus-based vectors, including human immunodeficiency (HIV)-based vectors. See, e.g., Vigna and

Naldini, J. Gene Med. 5:308-316, 2000 and Miyoshi et al., J. Virol. 72:8150-8157, 1998. Lentiviral vectors are advantageous in that they are capable of infecting both actively dividing and non-dividing cells. They are also highly efficient at transducing human epithelial cells. Lentiviral vectors for use in the invention may be derived from human and non-human (including SUV) lentiviruses. A typical lentiviral vector includes nucleic acid sequences required for vector propagation as well as a tissue-specific promoter operably linked to a GRP nucleic acid.

[00130] A lentiviral vector may be packaged into any suitable lentiviral capsid. The substitution of one particle protein with another from a different virus is referred to as "pseudotyping". The vector capsid may contain viral envelope proteins from other viruses, including murine leukemia virus (MLV) or vesicular stomatitis virus (VSV). The use of the VSV G-protein yields a high vector titer and results in greater stability of the vector virus particles.

[00131] Alphavirus-based vectors, such as those made from semliki forest virus (SFV) and sindbis virus (SIN), might also be used in the invention. Use of alphaviruses is described in Lundstrom, K., Intervirology 43:247-257, 2000 and Perri et al., Journal of Virology 74:9802-9807, 2000. Alphavirus vectors typically are constructed in a format known as a replicon. A replicon may contain (1) alphavirus genetic elements required for RNA replication, and (2) a heterologous nucleic acid such as one encoding a GRP nucleic acid.

[00132] Recombinant, replication-defective alphavirus vectors are advantageous because they are capable of high-level gene expression, and can infect a wide host cell range. Alphavirus replicons may be targeted to specific cell types by displaying on their virion surface a functional ligand or binding domain that would allow selective binding to target cells expressing a cognate binding partner. Alphavirus replicons may establish latency, and therefore long-term heterologous nucleic acid expression in a host cell. The replicons may also exhibit transient heterologous nucleic acid expression in the host cell. To increase tissue selectivity of the virus and reduce risk not only can such a virus have a targeted ligand on the virion

surface, but also the heterologous nucleic acid (e.g., a GRP nucleic acid) can be operably linked to a tissue specific promoter.

[00133] In addition to viral vector-based methods, non-viral methods may also be used to introduce a GRP nucleic acid into a host cell. A review of non-viral methods of gene delivery is provided in Nishikawa and Huang, Human Gene Ther. 12:861-870, 2001. A non-viral gene delivery method according to the invention employs plasmid DNA to introduce a GRP nucleic acid into a cell. Plasmid-based gene delivery methods are generally known in the art and are described in references such as Ilan, Y., Curr. Opin. Mol. Ther. 1:116-120, 1999, Wolff, J. A., Neuromuscular Disord. 7:314-318, 1997 and Arztl, Z., Fortbild Qualitatssich 92:681-683, 1998.

[00134] Methods involving physical techniques for introducing a GRP nucleic acid into a host cell can be adapted for use in the invention. For example, the particle bombardment method of gene transfer utilizes an Accell device (gene gun) to accelerate DNA-coated microscopic gold particles into a target tissue, e.g., a cancer tissue. See, e.g., Yang et al., Mol. Med. Today 2:476-481 1996 and Davidson et al., Rev. Wound Repair Regen. 6:452-459, 2000. As another example, cell electroporation (also termed cell electroporation) may be employed to deliver GRP nucleic acids into cells. See, e.g., Preat, V., Ann. Pharm. Fr. 59:239-244 2001.

[00135] Synthetic gene transfer molecules can be designed to form multimolecular aggregates with plasmid DNA. These aggregates can be designed to bind to a target cell surface in a manner that triggers endocytosis and endosomal membrane disruption. Cationic amphiphiles, including lipopolyamines and cationic lipids, may be used to provide receptor-independent GRP nucleic acid transfer into target cells. In addition, preformed cationic liposomes or cationic lipids may be mixed with plasmid DNA to generate cell-transfecting complexes. Methods involving cationic lipid formulations are reviewed in Felgner et al., Ann. N.Y. Acad. Sci. 772:126-139, 1995 and Lasic and Templeton, Adv. Drug Delivery Rev. 20:221-266, 1996. For gene delivery, DNA may also be coupled

to an amphipathic cationic peptide (Fominaya et al., J. Gene Med. 2:455-464, 2000).

[00136] DNA microencapsulation may be used to facilitate delivery of a GRP nucleic acid. Microencapsulated gene delivery vehicles may be constructed from low viscosity polymer solutions that are forced to phase invert into fragmented spherical polymer particles when added to appropriate nonsolvents. Methods involving microparticles are discussed in Hsu et al., J. Drug Target 7:313-323, 1999 and Capan et al., Pharm. Res. 16:509-513, 1999.

[00137] Protein transduction offers an alternative to gene therapy for the delivery of therapeutic proteins into target cells, and methods involving protein transduction are within the scope of the invention. Protein transduction is the internalization of proteins into a host cell from the external environment. The internalization process relies on a protein or peptide which is able to penetrate the cell membrane. To confer this ability on a normally non-transducing protein, the non-transducing protein can be fused to a transduction-mediating protein such as the antennapedia peptide, the HIV TAT protein transduction domain, or the herpes simplex virus VP22 protein. See Ford et al., Gene Ther. 8:1-4, 2001.

[00138] There are two major approaches to getting the nucleic acid (optionally contained in a vector) into a subject's cells; *in vivo* and *ex vivo*. For *in vivo* delivery the nucleic acid is injected directly into the subject, usually at the site where the nucleic acid is needed. For *ex vivo* treatment, the subject's cells are removed, the nucleic acid is introduced into these isolated cells and the modified cells are administered to the subject either directly or, for example, encapsulated within porous membranes which are implanted into the subject (see, e.g., U.S. Pat. Nos. 4,892,538 and 5,283,187). There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell

fusion, DEAE-dextran, the calcium phosphate precipitation method, viral vectors and the like. A commonly used vector for *ex vivo* and *in vivo* delivery is a viral vector as discussed above.

[00139] Host cells can be transfected or transformed with expression or cloning vectors described herein and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the nucleic acids encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in *Mammalian Cell Biotechnology: a Practical Approach*, M. Butler, ed. (IRL Press, 1991) and Sambrook et al.

[00140] Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl_2 , CaPO_4 , liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., *supra*, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., *Gene*, 23:315 (1983) and WO 89/05859 published 29 Jun. 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, *Virology*, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Pat. No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., *J. Bact.*, 130:946 (1977) and Hsiao et al., *Proc. Natl. Acad. Sci. (USA)*, 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., *Methods in Enzymology*, 185:527-537 (1990) and Mansour et al., *Nature*, 336:348-352 (1988).

[00141] Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacter, Erwinia, Klebsiella, Proteus, Salmonella, e.g., Salmonella typhimurium, Serratia, e.g., Serratia marcescans, and Shigella, as well as Bacilli such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 Apr. 1989), Pseudomonas such as *P. aeruginosa*, and Streptomyces. These examples are illustrative rather than limiting.

[00142] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe*, Kluyveromyces hosts such as, e.g., *K. lactis*, *K. fragilis*, *K. bulgaricus*, *K. wickerhamii*, *K. waltii*, *K. drosophilae*, *K. thermotolerans*, and *K. marxianus*; *Yarrowia*; *Pichia pastoris*; *Candida*; *Trichoderma reesei*; *Neurospora crassa*; *Schwanniomyces* such as *Schwanniomyces occidentalis*; and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium*, and *Aspergillus* hosts such as *A. nidulans* and *A. niger*. Methylophilic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of Hansenula, Candida, Kluyveromyces, Pichia, Saccharomyces, Torulopsis, and Rhodotorula. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylophilic Yeasts, 269 (1982).

[00143] Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol. 36:59, 1977); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub et al., Proc.

Natl. Acad. Sci. USA 77:4216, 1980); mouse sertoli cells (TM4, Mather, Biol. Reprod. 23:243-251, 1980); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather et al., Annals N.Y. Acad. Sci. 383:44-68, 1982); MRC 5 cells; FS4 cells; and a human hepatoma line (Hep G2).

[00144] Host cells are transformed with the above-described GRP nucleic acid expression or cloning vectors and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the nucleic acids encoding the desired sequences.

[00145] The GRP nucleic acids (e.g., antisense, RNAi, ribozymes, variants, coding sequences and the like) may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

[00146] Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from

complex media, e.g., the gene encoding D-alanine racemase for Bacilli.

[00147] An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the BDB oligopeptide-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub *et al.*, Proc. Natl. Acad. Sci. USA, 77:4216, 1980. A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 (Stinchcomb *et al.*, Nature, 282:39, 1979; Kingsman *et al.*, Gene, 7:141, 1979; Tschemper *et al.*, Gene, 10:157, 1980). The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan.

[00148] A variety of well-known techniques can be used to identify polypeptides which specifically bind to, for example, GRP78 and/or caspase-7, and regulate their interactions. Exemplary techniques include mobility shift DNA-binding assays, methylation and uracil interference assays, DNase and hydroxy radical footprinting analysis, fluorescence polarization, and UV crosslinking or chemical cross-linkers. For a general overview, see, e.g., Ausubel (chapter 12, DNA-Protein Interactions). Furthermore, biological assays that measure the agonistic and antagonistic effects of such agents are also provided.

[00149] For example, the invention provides a screening assay to determine the GRP agonistic or antagonistic effect an agent may have on a cell. The assay comprises contacting a cell expressing a GRP with an agent suspected to have GRP agonist or antagonist activity. Contacting the cell with a chemotherapeutic agent (e.g., etoposide) and measuring the percent survival of the cell or cells in culture. Where cell survival is increased compared to a control, the agent has agonistic activity, wherein the cell survival is decreased the agent has antagonistic activity.

[00150] In another embodiment, the invention provides pharmaceutical compositions comprising an agent identified by a method of the invention, and instructions for use of the agent in the treatment of a cell proliferative disorder. For example, an agent identified as regulating the interaction between GRP78 and

a cytosolic component, or an agent that regulates the ability of GRP78 to integrate in to a membrane, such as an ER membrane, can be included in a pharmaceutical composition to treat a cell proliferative disorder. The treatment can encompass inhibiting the disorder by promoting apoptosis or by inhibiting apoptosis. For example, the methods of the invention are suitable for use in preventing dividing cells from further replication by promoting apoptosis or in preventing non-dividing cells from destruction by inhibiting apoptosis.

[00151] The invention provides methods and compositions for treating a subject having a cell proliferative disorder. The subject can be any mammal, and is preferably a human. The contacting can be in vivo or ex vivo. Methods of administering pharmaceutical compositions are known in the art and include, for example, systemic administration, topical administration, intraperitoneal administration, intra-muscular administration, as well as administration directly at the site of a tumor or cell-proliferative disorder and other routes of administration known in the art.

[00152] The pharmaceutical compositions according to the invention may be administered locally or systemically. By "therapeutically effective dose" is meant the quantity of a compound according to the invention necessary to prevent, to cure or at least partially arrest the symptoms of the disease and its complications. Amounts effective for this use will, of course, depend on the severity of the disease and the weight and general state of the subject. Typically, dosages used in vitro may provide useful guidance in the amounts useful for in situ administration of the pharmaceutical composition, and animal models may be used to determine effective dosages for treatment of particular disorders. Various considerations are described, e.g., in Langer, Science, 249: 1527, (1990); Gilman et al. (eds.) (1990), each of which is herein incorporated by reference.

[00153] As used herein, "administering a therapeutically effective amount" is intended to include methods of giving or applying a pharmaceutical composition of the invention to a subject that allow the composition to perform its intended therapeutic function. The therapeutically effective amounts will

vary according to factors such as the degree of infection in a subject, the age, sex, and weight of the individual. Dosage regimen can be adjusted to provide the optimum therapeutic response. For example, several divided doses can be administered daily or the dose can be proportionally reduced as indicated by the exigencies of the therapeutic situation.

[00154] As used herein, a "pharmaceutically acceptable carrier" is intended to include solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the pharmaceutical composition, use thereof in the therapeutic compositions and methods of treatment is contemplated. Supplementary active compounds can also be incorporated into the compositions.

[00155] The principal pharmaceutical composition is compounded for convenient and effective administration in effective amounts with a suitable pharmaceutically acceptable carrier in an acceptable dosage unit. In the case of compositions containing supplementary active ingredients, the dosages are determined by reference to the usual dose and manner of administration of the said ingredients.

[00156] Further, methods of the invention can be performed alone or in conjunction with standard medical treatments currently available for treating a cell proliferative disorder. For example, when a tumor is being treated, it may be preferable to remove the majority of a tumor surgically or by radiation prior to introducing a construct of the invention in to the cells comprising the tumor.

[00157] The terms "protein", "peptide" and "polypeptide" as used herein, describe any chain of amino acids, regardless of length or post-translational modification (for example, glycosylation or phosphorylation). Thus, the terms can be used interchangeably herein to refer to a polymer of amino acid residues. The terms also apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid. Thus, the term

"polypeptide" includes full-length, naturally occurring proteins as well as recombinantly or synthetically produced polypeptides that correspond to a full-length naturally occurring protein or to particular domains or portions of a naturally occurring protein. The term also encompasses mature proteins which have an added amino-terminal methionine to facilitate expression in prokaryotic cells.

[00158] Polypeptides and peptides can be chemically synthesized using known techniques or produced using known molecular biology techniques. Polypeptides and proteins are encoded in the genome of an organism by nucleic acids in discrete functional units sometimes referred to as "genes". Nucleic acid molecules, however, can be removed and isolated from their naturally occurring environment and engineered and manipulated using molecular biology techniques. The term "isolated" means altered "by the hand of man" from its natural state; i.e., if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a naturally occurring nucleic acid molecule or a polypeptide naturally present in a living animal in its natural state is not "isolated", but the same nucleic acid or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein.

[00159] "Polynucleotide" or "nucleic acid molecule" refers to a polymeric form of nucleotides at least 10 bases in length. By "isolated nucleic acid" is meant a polynucleotide that is not immediately contiguous with either of the coding sequences with which it is immediately contiguous (one on the 5' end and one on the 3' end) in the naturally occurring genome of the organism from which it is derived. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector; into an automatically replicating plasmid or virus; or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA) independent of other sequences. The nucleic acid molecules of the invention may comprise ribonucleotides, deoxyribonucleotides, or modified forms of either nucleotide. The term includes single and double stranded forms.

[00160] The term nucleic acid molecule(s) or polynucleotide(s) generally refers to any polyribonucleotide or polydeoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. Thus, for instance, polynucleotides as used herein refers to, among others, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions.

[00161] In addition, a polynucleotide or nucleic acid molecule as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide.

[00162] As used herein, the term polynucleotide includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "nucleic acid molecules" as that term is intended herein.

[00163] Nucleic acid molecules comprising an antisense molecule, a siRNA molecule, or encoding a GRP polypeptide and the like, as disclosed herein, can be operatively linked to expression control element(s). "Operatively linked" refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. An expression control element(s) operatively linked to a nucleic acid molecule of the invention is ligated such that transcription of the nucleic acid molecule is achieved under conditions compatible with the expression control element(s). As used herein, the term "expression control element(s)" refers to control domain that regulate the expression of a nucleic acid molecule to which it is operatively linked. Expression control element(s) are operatively linked to a nucleic acid molecules

when the expression control element(s) control and regulate the transcription and, as appropriate, translation of the nucleic acid molecule. Thus, expression control element(s) can include appropriate promoters, enhancers, transcription terminators, a start codon (i.e., ATG) in front of a protein-encoding nucleic acid, splicing signals for introns, maintenance of the correct reading frame of that gene to permit proper translation of the mRNA, and stop codons. The term "control element(s)" is intended to include, at a minimum, components whose presence can influence expression, and can also include additional components whose presence is advantageous, for example, leader sequences and fusion partner sequences. Expression control element(s) can include a promoter.

[00164] By "promoter" is meant a minimal nucleic acid domain sufficient to direct transcription. Also included in the invention are those promoter elements which are sufficient to render promoter-dependent gene expression controllable for cell-type specific, tissue-specific, or inducible by external signals or agents; such elements may be located in the 5' or 3' regions of the gene. Both constitutive and inducible promoters, are included in the invention (see e.g., Bitter et al., Methods in Enzymology 153:516-544, 1987). For example, when cloning in bacterial systems, inducible promoters such as pL of bacteriophage- γ , plac, ptrp, ptac (ptrp-lac hybrid promoter) and the like may be used. When cloning in mammalian cell systems, promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the retrovirus long terminal repeat; the adenovirus late promoter; the vaccinia virus 7.5K promoter) may be used. Promoters produced by recombinant DNA or synthetic techniques may also be used to provide for transcription of the nucleic acids of the invention.

[00165] A nucleic acid molecule may be designed to selectively hybridize to a target polynucleotide or oligonucleotide under desired conditions. The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture.

[00166] The phrase "stringent hybridization conditions" refers to conditions under which a nucleic acid molecule will hybridize to its target complementary sequence, typically in a complex mixture of nucleic acids, but to no other sequences. In the context of the invention, stringent conditions comprises hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Typically, the conditions are such that sequences at least about 65%-70% or 75% or more homologous to each other typically remain hybridized to each other.

[00167] Generally, stringent conditions are selected to be about 5 to 10 °C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the nucleic acid molecules complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30 °C for short probes (for example, 10 to 50 nucleotides) and at least about 60 °C. for long probes (for example, greater than 50 nucleotides). Stringent conditions also may be achieved with the addition of destabilizing agents, for example, formamide.

[00168] Exemplary highly stringent hybridization conditions can be as following, for example: 50% formamide, 5xSSC and 1% SDS, incubating at 42 °C, or 5xSSC and 1% SDS, incubating at 65 °C, with wash in 0.2xSSC and 0.1% SDS at 65 °C. Alternative conditions include, for example, conditions at least as stringent as hybridization at 68 °C for 20 hours, followed by washing in 2xSSC, 0.1% SDS, twice for 30 minutes at 55 °C and three times for 15 minutes at 60 °C. Another alternative set of conditions is hybridization in 6xSSC at about 45 °C, followed by one or more washes in 0.2xSSC, 0.1% SDS at 50-65 °C. Exemplary moderately stringent hybridization conditions include a hybridization in a

buffer of 40% formamide, 1 M NaCl, 1% SDS at 37 °C, and a wash in 1xSSC at 45 °C.

[00169] "Treating" or "treatment" or "alleviation" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented. A subject or mammal is successfully "treated" for a neoplastic disorder/cancer if, after receiving a therapeutic amount of a GRP antagonist the subject shows observable and/or measurable reduction in or absence of one or more of the following: reduction in the number of cancer cells or absence of the cancer cells; reduction in the tumor size; inhibition (i.e., slow to some extent and preferably stop) of cancer cell infiltration into peripheral organs including the spread of cancer into soft tissue and bone; inhibition (i.e., slow to some extent and preferably stop) of tumor metastasis; inhibition, to some extent, of tumor growth; and/or relief to some extent, one or more of the symptoms associated with the specific cancer; reduced morbidity and mortality, and improvement in quality of life issues.

[00170] The phrase "non-dividing" cell refers to a cell that does not go through mitosis. Non-dividing cells may be blocked at any point in the cell cycle, (e.g., G0/G1, G1/S, G2/M), as long as the cell is not actively dividing. Examples of pre-existing non-dividing cells in the body include neuronal, muscle, liver, skin, heart, lung, and bone marrow cells, and their derivatives.

[00171] By "dividing" cell is meant a cell that undergoes active mitosis, or meiosis. Such dividing cells include stem cells, skin cells (e.g., fibroblasts and keratinocytes), gametes, and other dividing cells known in the art. Of particular interest and encompassed by the term dividing cell are cells having cell proliferative disorders, such as neoplastic cells. The term "cell proliferative disorder" refers to a condition characterized by an abnormal number of cells. The condition can include both hypertrophic (the continual multiplication of cells

resulting in an overgrowth of a cell population within a tissue) and hypotrophic (a lack or deficiency of cells within a tissue) cell growth or an excessive influx or migration of cells into an area of a body. The cell populations are not necessarily transformed, tumorigenic or malignant cells, but can include normal cells as well.

[00172] Cell proliferative disorders include disorders associated with an overgrowth of connective tissues, such as various fibrotic conditions, including scleroderma, arthritis and liver cirrhosis. Cell proliferative disorders include neoplastic disorders such as head and neck carcinomas. Head and neck carcinomas would include, for example, carcinoma of the mouth, esophagus, throat, larynx, thyroid gland, tongue, lips, salivary glands, nose, paranasal sinuses, nasopharynx, superior nasal vault and sinus tumors, esthesioneuroblastoma, squamous cell cancer, malignant melanoma, sinonasal undifferentiated carcinoma (SNUC) or blood neoplasia. Also included are carcinoma's of the regional lymph nodes including cervical lymph nodes, prelaryngeal lymph nodes, pulmonary juxtaesophageal lymph nodes and submandibular lymph nodes (Harrison's Principles of Internal Medicine (eds., Isselbacher, et al., McGraw-Hill, Inc., 13th Edition, pp1850-1853, 1994). Other cancer types, include, but are not limited to, lung cancer, colon-rectum cancer, breast cancer, prostate cancer, urinary tract cancer, uterine cancer lymphoma, oral cancer, pancreatic cancer, leukemia, melanoma, stomach cancer and ovarian cancer.

[00173] Methods involving conventional molecular biology techniques are described herein. Such techniques are generally known in the art and are described in detail in methodology treatises such as Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, ed. Sambrook et al., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989; and Current Protocols in Molecular Biology, ed. Ausubel et al., Greene Publishing and Wiley-Interscience, New York, 1992 (with periodic updates). Various techniques using polymerase chain reaction (PCR) are described, e.g., in Innis et al., PCR Protocols: A Guide to Methods and Applications, Academic Press: San Diego, 1990. PCR-primer pairs can be derived from known sequences by known

techniques such as using computer programs intended for that purpose (e.g., Primer, Version 0.5, 81991, Whitehead Institute for Biomedical Research, Cambridge, Mass.). Methods for chemical synthesis of nucleic acids are discussed, for example, in Beaucage and Carruthers, Tetra. Letts. 22:1859-1862, 1981, and Matteucci et al., J. Am. Chem. Soc. 103:3185, 1981. Chemical synthesis of nucleic acids can be performed, for example, on commercial automated oligonucleotide synthesizers. Immunological methods (e.g., preparation of antigen-specific antibodies, immunoprecipitation, and immunoblotting) are described, e.g., in Current Protocols in Immunology, ed. Coligan et al., John Wiley & Sons, New York, 1991; and Methods of Immunological Analysis, ed. Masseyeff et al., John Wiley & Sons, New York, 1992. Conventional methods of gene transfer and gene therapy can also be adapted for use in the invention. See, e.g., Gene Therapy: Principles and Applications, ed. T. Blackenstein, Springer Verlag, 1999; Gene Therapy Protocols (Methods in Molecular Medicine), ed. P. D. Robbins, Humana Press, 1997; and Retro-vectors for Human Gene Therapy, ed. C. P. Hodgson, Springer Verlag, 1996.

[00174] A few diseases and disorders (e.g., ischemia and neoplastic disorders) have been mentioned. However, those of skill in the art will recognize that a variety of diseases and degenerative disorders involve aberrant or dysregulated apoptosis, resulting in inappropriate or premature cell death or inappropriate cell proliferation. For example, inhibition of cell death may contribute to disease in the immune system by allowing the persistence of self-reactive B and T cells, which leads to autoimmune disease. Furthermore, the infection by certain viruses may depend on suppression of host cell death by anti-apoptotic viral gene products and inhibition of apoptosis can alter the course (lytic vs. latent) of viral infection.

EXAMPLES

[00175] The invention is based, in part, on the discovery that GRPs (e.g., GRP78) confers resistance to topoisomerase inhibitors through protection against drug-induced apoptosis. As shown in Figure 1, panel A, quantitation of the immunoblots of whole cell extracts showed 5-fold higher GRP78 level in C.1 cells compared with the parental CHO cells, whereas the level of GRP94, also an

ER-localized chaperone protein, and a 45-kDa unidentified protein (X) recognizable by the anti-KDEL antibody was relatively constant in both cell lines. *In situ* immunofluorescence imaging using anti-GRP78 antibody further revealed that in both CHO and C.1 cells, the majority of GRP78 was concentrated in the perinuclear region, consistent with its location in the ER (Figure 1, Panel B). The intensity of the immunofluorescent signal for GRP78 was greater in the majority of C.1 cells compared with CHO cells.

[00176] In examining the distribution of GRP78 and caspase-7 *in situ* using immunofluorescence, caspase-7 exhibits a perinuclear pattern indicative of ER localization (Figure 1, Panel C). Confocal microscopy further revealed caspase-7 is in close proximity with a subfraction of GRP78. The co-localization of GRP78 and caspase-7 was primarily detected in the perinuclear/ER region.

[00177] The physical interaction of endogenous caspase-7 with GRP78 was further confirmed using whole cell extracts prepared from CHO and C.1 cells. In agreement with the co-localization results obtained from confocal microscopy, procaspase-7 forms a complex with a high level of GRP78 in C.1 cells (Figure 6, Panel A, lane 2). For CHO cells, GRP78 was detected as a faint band in the anti-caspase-7 immunoprecipitate using an anti-KDEL antibody (Figure 6, Panel A, lane 1), and the signal for GRP78 was very enhanced when an anti-hamster GRP78 antibody was used for the Western blots (Figure 6, Panel B, lane 1). Using anti-caspase-3 as the immunoprecipitating antibody, GRP78 was not detected associated with procaspase-3 in Western blots (Figure 6, Panel A, lanes 3 and 4). Thus, endogenous GRP78 constitutively associates with procaspase-7. While the data provided herein indicates that GRP78 and caspase-7 interact, the invention is not limited to a direct interaction between the two proteins. It is understood that the invention encompasses a cytosolic component that is a complex of polypeptides, including caspase-7, or caspase-7 individually. By preventing the interaction of GRP78 with caspase, the agent modulates apoptosis by promoting apoptosis. Alternatively, by promoting the interaction of GRP78 with

caspase-7, an agent would modulate apoptosis by inhibiting apoptosis.

[00178] As shown in Figure 7, Panel A, at low dose of trypsin digestion, a resistant carboxyl band of about 35kDa was detected. At the higher dose of trypsin, the intensity of the 35-kDa band became stronger, and a minor band of around 50-kDa was also visible. The digestion pattern for the CHO cells was the same, with the resistant bands more prominent for C.1 cells correlating with GRP78 overexpression. The trypsin treatment did not digest ER proteins localized inside the ER lumen as confirmed by the calreticulin control (Figure 7, Panel B).

[00179] In addition, sodium carbonate extraction of the microsome membrane fractions indicates that GRP78 is located in both the membrane and luminal (Figure 7, Panel C). These results show that GRP78 is not exclusively an ER lumen protein, rather a subpopulation exist as a transmembrane protein. This is consistent with domains III and IV serving as putative transmembrane domains, with carboxyl fragments locating inside the lumen of the ER rendering them resistant to trypsin digestion (Figure 7, Panel A). This topology further indicates that part of GRP78 is exposed to the cytosol, allowing it to interact with cytosolic components. Thus, in another embodiment, the invention provides a method of modulating apoptosis by contacting glucose regulated protein 78 (GRP78) with an agent that inhibits or prevents the ability of the protein to integrate in to the membrane of the endoplasmic reticulum. In yet another embodiment, the invention provides a method of identifying an agent that modulates the interaction of glucose regulated protein 78 (GRP78) with a membrane by providing a polypeptide that includes hydrophobic transmembrane domain III (amino acids 210-260 of SEQ ID NO:1 or 2) and/or domain IV (amino acids 400-450 of SEQ ID NO:1 or 2) of the protein of glucose regulated protein 78. The polypeptide can be contacted with an agent, and the effect of the agent on the interaction can be determined. Agents that regulate the ability of the polypeptide to integrate in to the membrane are candidates for modulating apoptosis. For example, an agent that inhibits the ability of GRP78 to integrate in to the membrane will also be capable of promoting apoptosis because

it will prevent GRP78 from interacting with cytosolic components that are required to promote apoptosis.

[00180] It was further determined that the ATP-binding domain of GRP78 is necessary for the interaction with cytosolic components. The ATP binding domain resides in the amino portion of GRP78 (Figure 6, Panel C). The invention further encompasses the use of fragments of GRP78 containing the ATP-binding domain in the methods of the invention. For example, a polypeptide that includes amino acids 125-275 of SEQ ID NO:1 or 2, or amino acids 150-250 of SEQ ID NO:1 or 2, or amino acids 175-201 of SEQ ID NO:1 or 2 can be used in a method to identify an agent that regulates the interaction of GRP78 and cytosolic components.

[00181] CHO cell line AD-1 that stably expresses a deleted form of GRP78 (Figure 6, Panel C) was used to determine that the ATP-binding region of GRP78 is necessary for binding to caspase. The deletion spans residues 175 to 201 within the ATP binding domain, resulting in defective ATPase activity. Western blot analysis of whole cell extracts prepared from CHO and AD-1 cells confirmed expression of the deleted GRP78 form, in addition to endogenous wild-type GRP78, in AD-1 cells (Fig. 6B, lanes 3 and 4).

[00182] Immunoprecipitation using anti-caspase-7 antibody showed that whereas procaspase-7 is able to form a complex with wild-type GRP78, deletion of residues 175 to 201 abolished its ability to bind to procaspase-7 (Figure 6, Panel B, lanes 1 and 2. Upon etoposide treatment, AD-1 cells showed more caspase-7 activation *in vivo* and more extensive DNA fragmentation compared with C.1 cells that overexpress the wild-type protein (Figure 8, Panels A and B). Annexin labeling and clonogenic survival assays performed with AD-1 cells further showed no protection against etoposide treatment compared with the parental CHO cells.

[00183] A transient transfection cell death assay further indicated that inhibition of apoptosis by GRP78 was dependent upon the GRP78-caspase interaction. Cell viability was measured quantitatively by the retention of β -galactosidase activity in the cells after drug treatment. As shown in Figure 8, cells transfected with the expression vector for wild-type GRP78 conferred protection against etoposide treatment. To confirm

that the ATP binding function of GRP78 is required for the protective effect of GRP78, the cells were transfected with vectors expressing either wild-type GRP78 or mutant GRP78 (G227D), which carries an amino acid substitution at position 227, destroying its ATP binding ability. As shown in Figure 8, Panel C, the protective effect was lost with the mutant form of GRP78.

[00184] Experiments were performed to look at the effect of GRP78 on chemotherapeutics. A strong cellular promoter (CMV) was used to drive expression of GRP78 in the context of a well-characterized adenovirus vector called pShuttle-CMV. Both the sense and antisense orientation of GRP78 were constructed, to serve the function of overexpression or suppression of GRP78. Two versions of adenovirus with CMV promoter driving antisense (AS) Grp78 were constructed (see Figures 11A-C). The construction scheme for the full length AS construct is shown in Figure 11. An adenovirus construct expressing a partial length AS comprising a 320 bp fragment of the grp78 exon I was cloned in reverse orientation to the CMV promoter (see Fig. 11C). This shorter fragment targets the AUG start codon and may be more effective than the full length antisense molecule.

[00185] Overexpression of the His-tagged GRP78 in a human 293T tissue culture test system was performed. This cell line was used because it can be infected very efficiently with adenovirus. For this purpose, different doses of adenovirus expressing His-tagged GRP78 was infected into 293T cells. After 72 hr, the cell lysate was prepared and immunoblot was performed to detect the level of His-tagged GRP78, using antibody against the His-tagged which is specific for the adenovirus expressed protein. The results showed that His-tagged GRP78 was expressed in high levels in a dosage dependent manner (Figure 12, lanes 4, 5 and 6). This proves that the adenovirus construct for expressing full length GRP78 is successful. The next step is to repeat these experiments in MDA and MCF-7 cells. This step is more difficult because the cells are harder to culture and they are more difficult to infect.

[00186] As a proof of principle, the two antisense (AS) constructs were tested to determine their ability to suppress the His-tagged GRP78 in the human 293T tissue culture test system.

For this purpose, different doses of adenovirus expressing either the full length AS or 320 bp AS was co-infected with adenovirus expressing His-tagged GRP78 into 293T cells. After 72 hr, the cell lysate was prepared and immunoblot was performed to detect the level of His-tagged GRP78, using antibody against the His-tagged which is specific for the adenovirus expressed protein. The results showed that both the full length AS (Figure 12, lanes 7, 8 and 9) and the 320 bp AS (Figure 12, lanes 1, 2 and 3) were able to suppress expression of the His-tagged GRP78 in a dosage dependent manner. This proves that the adenovirus constructs for expressing antisense GRP78 are successful. The most drastic reduction was obtained with the 320 bp AS (Figure 12, lane 1).

[00187] Next human breast cancer MDA-MB-435 cells were infected with the adenovirus expressing the 320 bp AS, in the presence or absence of treatment with the chemotherapy drug etoposide. The same cells were infected with the GFP negative control adenovirus. The results showed that in the mock-infected cells, etoposide treatment by itself reduced the amount of endogenous GRP78 by about 40% (Figure 13, lanes 1 and 2). Importantly, the 320 bp AS construct further reduced GRP78 level significantly, particularly in cells treated with etoposide, such that the final level was less than 10% (Figure 13, lanes 3 and 4). Thus, both the full length and the 320 bp version of the AS construct targeted against GRP78 blocked expression of GRP78 in a 293T test system. This was repeated in human breast cancer cells and showed that the AS adenovirus is able to suppress endogenous GRP78 expression.

[00188] Experiments were also performed to determine the anti-apoptotic effect conferred by overexpression of GRP78. This task was completed. GRP78 overexpression confers resistance to all four drugs (cisplatin, doxorubicin, etoposide and camptothecin). The results are summarized in Table 2.

Table 2

	% Survival (Colony Assay)	
	Control	GRP78 Overexpression
Cisplatin (μ M)		
0	100	100
3.3	43	60
6.6	3.7	50
9.9	0	27
13.0	0	16

Doxorubicin (µg/ml)		
0	1	100
0.2	80	95
0.4	42	84
0.6	2	68
0.8	0	48
1.0	0	32
Etoposide (µM)		
0	100	100
0.2	71	93
0.4	67	93
0.8	26	77
1.6	1.5	63
Camptothecin (ng/ml)		
0	100	100
5	68	82
20	0.7	22
60	0	2

[00189] The antisense approach described above was replaced with an siRNA approach. The sequence of the Grp78 siRNA included:

5' AAGGTTACCCATGCAGTTGTT 3' (SEQ ID NO:4)
 3' TTCCAATGGGTACGTCAACAA 5' (SEQ ID NO:17)

When blasted against the human genomic sequence, this sequence is unique and in principle, should not affect any other human gene. To prove this, experiments were performed to test the effect of this siRNA on the expression of GRP78 and related stress proteins GRP94 and HSP70 in human 293T cells. The level of β -actin was used as loading control. As shown in Figure 14, only GRP78 level is suppressed, confirming that the siRNA is specific for GRP78.

[00190] Experiments further showed that Grp78(II) siRNA at 80 nM or higher can significantly suppress GRP78 level in human breast cancer MDA-MB-435 cells (Figure 15). This translates to more death in the cells treated with Grp78(II) siRNA than control siRNA targeted against the unrelated green fluorescence protein (Figure 16).

[00191] One candidate target of GRP78 action is BIK, the BH3-only protein inducible in response to DNA damage that is located in the ER as well as the mitochondria. Remarkably, ER-targeted BIK can induce cytochrome c release, suggesting it can act at the ER site to initiate a parallel cell death pathway (Germain et al., 2002). To test whether GRP78, as a molecular chaperone, can either directly or indirectly block the action of pro-apoptotic molecules that control the release of cytochrome c from the mitochondria the following experiment was performed. Using 293T

as a model system, BIK level was observed to increase following etoposide treatment and co-IP of GRP78 with endogenous BIK (Figure 17A). These results suggesting that GRP78 overexpression can protect cells from cell death mediated by ER-targeted BIK (Figure 17B). These findings imply that in cells treated with etoposide, there are both physical and functional interactions between BIK and GPP78. Thus, this can contribute in part to the protective effect of GRP78 towards etoposide-induced cell death.

[00192] Cell Culture Conditions - The CHO cells were maintained in α -minimum Eagle's medium with nucleosides supplemented with 10% dialyzed fetal calf serum and 1% penicillin/streptomycin/neomycin antibiotics. The C.1 and AD-1 cells were maintained in the above conditions in the presence of 0.1 μ g/ml methotrexate but without added nucleosides. The establishment of stable T24/83 human transitional bladder carcinoma cell lines overexpressing human GRP78 or transfected with the empty expression vector (pcDNA3.1) has been described. The T24/83 cell lines were maintained in M199 medium supplemented with 10% fetal calf serum containing 1% penicillin/streptomycin/neomycin antibiotics and 200 μ g/ml G418. The human acute T cell leukemia Jurkat cells were maintained in RPMI 1640 medium supplemented with 10% fetal calf serum containing 1% penicillin/streptomycin/neomycin antibiotics. All the cells were maintained at 37°C in a humidified atmosphere of 5% CO₂/95% air.

[00193] Reagents - Etoposide (Calbiochem) was dissolved in Me₂SO at a concentration of 30 mM and stored at -20 °C. Methotrexate (Sigma) was dissolved in a minimum amount of 1 M NaOH, diluted with water to 1 μ g/ml, and stored at -20°C. Doxorubicin (Bedford Laboratories, Bedford, OH) at 2 mg/ml and camptothecin (Amersham Biosciences) at 20mg/ml were supplied as isotonic solutions.

[00194] Cell Cycle Analysis - Following seeding, exponentially growing cells were trypsinized at different days and fixed in 70% ethanol. The fixed cells were treated with PBS containing 0.1% (v/v) Triton X-100, 0.2 mg/ml DNase-free RNase, and 20 μ g/ml propidium iodide (PI) for 30 min at room temperature. The cell cycle distributions were analyzed by fluorescence-activated cell

sorting (FACS) analysis (FACstar; BD Biosciences). The cell cycle distribution measurements were repeated three to four times.

[00195] Clonogenic Survival Assays - Four thousand cells were seeded into 10-cm-diameter dishes. Two days after seeding, cells were treated with etoposide for 6 h, doxorubicin for 1 h, or camptothecin for 24 h at different concentrations as indicated. After drug treatment, the cells were grown in fresh medium for 10 to 14 days. The colonies were washed with ice-cold PBS, fixed with methanol, and stained with 10% Giemsa staining solution. The surviving fraction was determined by dividing the number of the surviving colonies in the drug-treated cells by the number of colonies in the non-treated control groups.

[00196] Annexin V Staining and FACS Analysis - CHO, C.1, and T24/83 cells were trypsinized, washed twice with ice-cold PBS, pH 7.4, and resuspended in 1 μ binding buffer (10 mM HEPES, pH 7.4, 140 mM NaCl, 2.5 mM CaCl₂ at a concentration of 1 x 10⁶ cells/ml. One hundred μ l of cell suspension was transferred to 5-ml plastic tubes, and 5 μ l of annexin V-fluorescein isothiocyanate (PharMingen) and 4 μ l of 0.5 mg/ml PI were added. The cells were gently vortexed and incubated in the dark at room temperature for 20 min. Four hundred μ l of binding buffer was added to each tube, and annexin V staining was analyzed by flow cytometry within 1 h. Cells negative for both PI and annexin V staining are live cells, annexin V positive staining cells are early apoptotic cells, and PI positive and annexin V positive staining cells are primarily cells in late stages of apoptosis.

[00197] Caspase-7 Activation Assays - The cells were either non-treated or treated with 100 μ M etoposide for 6 h and harvested after 24 h. The cells were suspended in 5 volumes of a hypotonic buffer (5 mM Tris-HCl, pH 7.4, 5 mM KCl, 1.5 mM MgCl₂, 0.1 mM EGTA, pH 8.0, and 1 mM dithiothreitol) in the presence of 2 μ g/ml leupeptin, pepstatin, and aprotinin protease inhibitors. After incubation on ice for 20 min, sucrose was added to a final concentration of 250 mM, and the cells were disrupted by douncing eight times in a 1-ml Wheaton Dounce homogenizer. The homogenate was centrifuged twice at 750 μ g for 10 min. The supernatant was clarified again at 16,000 x g for 15 min at 4 °C and designated

as the cytoplasmic fraction. For *in vitro* caspase-7 activation assay, 150 µg of cell-free extract was incubated with various amounts of cytochrome c and dATP at 37 °C for 1 h. Equal amounts of total proteins were separated, and Western blotting was performed for caspase-7.

[00198] Western Blotting - The cell lysate was prepared in radioimmune precipitation assay buffer and subjected to immunoblot with antibodies against GRP78, GRP94, topoisomerase II, caspase-7, and α -actin as described. Nitrocellulose membranes containing the transferred proteins were blocked in Tris-buffered saline containing 5% non-fat dry milk and 0.1% Tween 20 for 1 h at room temperature and were probed with the respective primary antibodies. For GRP78, an anti-KDEL mouse monoclonal antibody (SPA-827), an anti-GRP78 rabbit polyclonal antibody directed against the carboxyl ten amino acids of rat GRP78 (SPA-826) (StressGen, Victoria, Canada), or an anti-hamster GRP78 rabbit polyclonal antibody at 1:3000, 1:2000, and 1:5000 dilution, respectively, was used. Dilutions for the other primary antibodies were as follows: anti-calnexin rabbit polyclonal antibody (SPA-865) (StressGen) at 1:2000, anti-calreticulin rabbit polyclonal antibody (SPA-600) (StressGen) at 1:3000, anti- β -actin mouse monoclonal antibody (Sigma) at 1:5000, anti-caspase-7 mouse monoclonal antibody (10-1-62) (BD Biosciences) at 1:1000, anti-caspase-3 rabbit polyclonal antibody (Cell Signaling, Beverly, MA) at 1:1000, and anti-topoisomerase II mouse monoclonal antibody (SWT3D1) (Oncogene, San Diego, CA) at 1:1000. Respective horseradish peroxidase-conjugated secondary antibodies were used, and the protein bands were visualized by the ECL method (Amersham Biosciences).

[00199] Transient Transfection Death Assay - Briefly, Jurkat cells were transiently transfected with either CMV-neo-Bcl2 or expression vectors for wild-type hamster GRP78 or a GRP78 ATP-binding site mutant G227D. After drug treatment, cell lysates were prepared and assayed for β -galactosidase activity remaining in the surviving cells. The percent cytotoxicity was calculated as described previously.

[00200] DNA Fragmentation Assays - The cells were either non-treated or treated with 100 µM etoposide for 12 h and harvested

after 48 h. The DNA fragmentation assays were performed using an apoptosis DNA ladder kit (Roche Molecular Biochemicals) according to manufacturer's instructions.

[00201] Immunofluorescence Staining and Image Analysis - CHO and C.1 cells were grown to 60% confluence in chamber slides (Nalge Nunc International, Naperville, IL), washed twice with PBS, and fixed with 4% paraformaldehyde in PBS for 10 min. The cells were then washed with PBS and permeabilized in PBS containing 0.1% Triton X-100 and 5% bovine serum albumin for 30 min. For detection of GRP78, the cells were stained with a 1:1000 dilution of anti-GRP78 (C-20) goat polyclonal antibody (Santa Cruz Biotechnology, Inc., Santa Cruz, CA) and a 1:500 dilution of anti-goat Texas red-conjugated secondary antibody (Vector Labs, Burlingame, CA). For detection of caspase-7, the cells were stained with anti-caspase-7 mouse monoclonal antibody (BD Biosciences) at a 1:500 dilution and a 1:500 dilution of anti-mouse fluorescein isothiocyanate-conjugated secondary antibody (Vector Labs). Cells were mounted in Vectashield with DAPI mounting medium (Vector Labs) and visualized on a Zeiss LSM 510 dual-photon confocal microscope. The T24/83 cells were incubated with the same anti-GRP78 polyclonal antibody as described for the CHO cells. Whole cell images were subsequently captured and analyzed using Northern exposure image analysis/archival software (Mississauga, Ontario, Canada).

[00202] Co-immunoprecipitation Assays - 2×10^6 cells were lysed in 400 μ l of extraction buffer (50 mM Tris-HCl, pH 7.5, 150 mM NaCl, 0.5% Nonidet P-40, and 0.5% deoxycholate, with protease inhibitor tablet (Roche Molecular Biochemicals)) and frozen and thawed three times. 500 μ g of total protein extract from each sample was pretreated with 50 μ l of protein A-Sepharose beads (Sigma) for 1 h at 4 °C prior to incubation with 5 μ g of either anti-caspase-7 mouse monoclonal antibody or anticaspase-3 antibodies for 2 h. Following the incubation period, 50 μ l of protein A-Sepharose beads was added, and the mixtures were rotated at 4 °C overnight. The beads were then washed five times with the extraction buffer. The immunoprecipitate was released from the washed beads by the addition of 30 μ l of 1x SDS-PAGE sample loading buffer (50 mM Tris-HCl, pH 6.8, 100 mM

dithiothreitol, 2% SDS, 0.1% bromphenol blue, 10% glycerol), followed by heating at 100 °C for 10 min. The supernatant obtained after centrifugation was resolved by SDS-PAGE and subjected to Western blot analysis to detect the co-immunoprecipitated proteins.

[00203] Isolation of Microsomes and Protease Digestion - The cells were trypsinized, and after washing with cold PBS, were lysed by incubation in 10 volumes of cold hypotonic buffer (10 mM Tris-HCl, pH 7.4), followed by Dounce homogenization. The lysate was immediately adjusted to 0.25 M sucrose, 1 mM MgCl₂ and centrifuged at 1000 x g for 10 min at 4 °C to remove nuclei and cell debris. The supernatant was further centrifuged at 100,000 x g for 90 min. The pellet, representing microsomes, was rinsed briefly with cold water and resuspended in 50 mM Tris-HCl, pH 7.4, and used for proteolytic digestion and sodium-carbonated extraction studies.

[00204] Sodium Carbonate Extraction-For separation of ER membranes from luminal proteins, the microsome pellet was resuspended in 50 volumes of 100 mM sodium carbonate, pH 11.5, and incubated on ice for 1 h. The suspension was then centrifuged for 1 h at 240,000 x g at 4 °C. The pellet, which represents ER membrane, was rinsed with cold water and resuspended in 1x SDS-PAGE sample loading buffer and analyzed by Western blot. Proteins present in the ER lumen were recovered from the supernatant by the addition of trichloroacetic acid to a final concentration of 10%. The pellet was washed three times with acetone, air-dried, solubilized in the 1x SDS-PAGE sample loading buffer, and analyzed by Western blot.

[00205] Limited Tryptic Digestion of Microsomal Proteins - For trypsin digestion reactions, the microsomes were incubated with trypsin (0.01% or 0.05%) for 30 min at room temperature. The proteolytic cleavage reactions were terminated by the addition of 1x SDS-PAGE sample loading buffer and boiling at 100 °C for 5 min. 10-20 µg of total protein from each reaction was analyzed by Western blot.

[00206] To examine directly whether specific overexpression of GRP78 can lead to the development of drug resistance, CHO and C.1 cells were exposed to various drugs, and cell survival was

measured using clonogenic survival assays. Various dosages of etoposide (also referred to as VP16), adriamycin (also referred to as doxorubicin), and camptothecin were tested. Both etoposide and adriamycin are inhibitors of topoisomerase II, and camptothecin is a topoisomerase I inhibitor. The results for each of the drugs tested are shown in Figure 2. With all three drugs, C.1 cells overexpressing GRP78 conferred higher resistance than CHO cells. These data establish that specific overexpression of GRP78, in the absence of the UPR, is sufficient to render CHO cells more resistant to topoisomerase I and II inhibitors.

[00207] To determine whether GRP78 protects the cells from etoposide-induced apoptosis, CHO and C.1 cells were either nontreated or treated with etoposide and labeled with annexin V and PI. The apoptotic cells were identified by annexin V labeling. For CHO cells, the percentage of apoptotic cells increased 10-fold (from 9 to 90%) upon etoposide treatment; for C.1 cells, the increase was 4.7-fold (from 15 to 70%) (Fig. 3A). More extensive DNA fragmentation was also detected in etoposide-treated CHO but not C.1 cells (Figure, Panel B).

[00208] A pair of stably transfected human transitional bladder carcinoma T24/83 cell lines selected and cultured under identical conditions, were used to determine the effect of GRP overexpression on neoplastic cells. The cell line, referred to as T24/83-GRP78, overexpressed human GRP78, and the other line, referred to as T24/83-pcDNA, was stably transfected with the empty expression vector pcDNA (28). Immunoblot analysis followed by normalization against α -actin revealed a 3-fold increase in the level of GRP78 expression in the T24/83-GRP78 cells as compared with T24/83-pcDNA cells (Fig. 4A, inset).

Overexpression of GRP78 in T24/83-GRP78 cells did not affect the expression level of ER chaperone proteins GRP94, protein disulfide isomerase and calreticulin, or heat shock protein HSP47 (Figure 4, Panel A). Whole cell imaging revealed much greater GRP78 immunofluorescence for the T24/83-GRP78 cells, confirming the results of the immunoblots (Figure 4, Panel B).

[00209] In agreement with the CHO cell lines, T24/83 cells overexpressing GRP78 exhibited more resistance to etoposide in

clonogenic survival assays (Figure, 4, Panel A). Similar protection was observed for adriamycin and camptothecin. For T24/83-cDNA cells, etoposide treatment increased the percentage of annexin V-labeled cells 2.7-fold (from 7 to 19%), as compared with an increase of 1.4-fold (from 8 and 11%) for T24/83-GRP78 cells (Fig. 4C).

[00210] With the availability of the GRP78 overexpressing cell lines, the effect of GRP78 overexpression on topoisomerase II level in the absence of an UPR was determined. CHO and C.1 cells were either non-treated or treated with etoposide, and the level of topoisomerase II was determined by immunoblotting (Figure 5, Panel A). The data indicate that specific GRP78 overexpression has no effect on the topoisomerase II protein level.

[00211] Analysis of the cell cycle distribution of exponentially growing cells showed CHO and C.1 cells with similar G1, S, and G2 distribution profiles (Figure 9). In contrast, CHO cells treated with tunicamycin or thapsigargin, both standard UPR inducers, showed more cells in G1 and a dramatic reduction in S phase cells. A similar pattern was observed for exponentially growing T24/83 cells. In both the vector-transfected and GRP78 overexpressing cells, the percentage of G1, S, and G2 cells is similar. Cells treated with tunicamycin or thapsigargin showed a higher percentage of G1 cells and a lower percentage in S phase (Figure 9). Collectively, these results show that in contrast to the UPR, specific overexpression of GRP78 does not alter the cell cycle distribution.

[00212] A number of embodiments of the invention have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the invention. Accordingly, other embodiments are within the scope of the following claims.

WHAT IS CLAIMED IS:

1. A method of modulating apoptosis in a cell, the method comprising contacting a glucose regulated protein (GRP) with an agent that regulates the interaction of the GRP with a cytosolic component that mediates apoptosis.
2. The method of claim 1, wherein the GRP is located in the endoplasmic reticulum.
3. The method of claim 1, wherein the GRP is GRP94 or GRP78.
4. The method of claim 1, wherein the GRP is GRP78.
5. The method of claim 1, wherein the cytosolic component that mediates apoptosis is a caspase.
6. The method claim 5, wherein the caspase is selected from the group consisting of Ced-3, caspase-1, caspase-2, caspase-4, caspase-5, caspase-6, caspase-7, caspase-8, caspase-9, caspase-10, and caspase 11-14.
7. The method of claim 6, wherein the caspase is caspase-7.
8. The method of claim 1, wherein the cytosolic component is a complex of polypeptides.
9. The method of claim 1, wherein the modulating is by inhibiting apoptosis.
10. The method of claim 9, wherein the method comprises contacting the cell with a nucleic acid encoding a GRP protein or functional fragment thereof.
11. The method of claim 10, wherein the GRP protein is GRP78.
12. The method of claim 10, wherein the nucleic acid is contained in an expression vector.
13. The method of claim 10, wherein the nucleic acid is operably linked to a control element.
14. The method of claim 13, wherein the control element is a promoter.
15. The method of claim 10, wherein the GRP78 fragment comprises an soluble fragment of GRP78 that interacts with the cytosolic component.
16. The method of claim 1, wherein the modulating is by promoting apoptosis.

17. The method of claim 16, wherein the modulating is by inhibiting the interaction of the GRP with the cytosolic component or inhibiting the production of GRP.
18. The method of claim 17, wherein the agent is a small molecule, a protein, a peptide, a peptidomimetic, a nucleic acid molecule or a combination thereof.
19. The method of claim 18, wherein the polypeptide is an antibody.
20. The method of claim 18, wherein the agent is a small molecule.
21. The method of claim 20, wherein the agent is versielostatin (VST), dATP or a combination thereof.
22. The method of claim 20, wherein the agent interacts with the ATP-binding domain of the protein.
23. The method of claim 22, wherein the agent is ATP, or derivative thereof, that binds to the ATP-binding domain of the protein.
24. The method of claim 23, wherein the ATP-binding domain comprises amino acids 125-275 of SEQ ID NO:2.
25. The method of claim 22, wherein the agent interacts with amino acids 150-250 of SEQ ID NO:2.
26. The method of claim 22, wherein the agent interacts with amino acids 175-201 of SEQ ID NO:2.
27. The method of claim 18, wherein the nucleic acid is an antisense molecule, a ribozyme, a siRNA, or a combination thereof.
28. The method of claim 27, wherein the antisense molecule interacts with a GRP78 polynucleotide.
29. The method of claim 27, wherein the siRNA interacts with a GRP78 polynucleotide.
30. The method of claim 28, wherein the antisense molecule comprises a sequence that is at least 80% identical to SEQ ID NO:1.
31. The method of claim 30, wherein the antisense molecule comprises a sequence that is at least 90% identical to SEQ ID NO:1.

32. The method of claim 30, wherein the antisense molecule comprises SEQ ID NO:3.
33. The method of claim 30, wherein the antisense molecule consists of SEQ ID NO:3.
34. The method of claim 29, wherein the siRNA comprises a sequence that is about 90% identical to SEQ ID NO:4 and its complement.
35. The method of claim 33, wherein the siRNA comprise a sequence that is about 95% identical to SEQ ID NO:4 and its complement.
36. The method of claim 29, wherein the siRNA comprises SEQ ID NO:4 and its complement.
37. The method of claim 28, wherein the siRNA consists of SEQ ID NO:4 and its complement.
38. The method of claim 27, wherein the nucleic acid is delivered to the cell in a vector.
39. The method of claim 1, wherein the cell is contacted *in vitro*.
40. The method of claim 1, wherein the cell is contact *in vivo*.
41. The method of claim 9, wherein the apoptosis results from a disease or disorder associated with stroke, heart attack, hypoxia, hypoglycemia, brain or spinal cord ischemia, or brain or spinal cord trauma.
42. The method of claim 1, wherein the modulating is promoting apoptosis and the cell is a neoplastic cell.
43. The method of claim 16, wherein the cell is a neoplastic cell.
44. A method of promoting apoptosis in a cell, the method comprising inhibiting glucose regulated protein 78 (GRP78) with an agent that (i) inhibits or prevents the ability of GRP78 to interact with a cytosolic protein and/or (ii) inhibits the production of GRP78.
45. The method of claim 44, wherein the agent is a polypeptide.
46. The method of claim 45, wherein the polypeptide is an antibody.
47. The method of claim 44, wherein the agent is a small molecule.

48. The method of claim 44, wherein the agent interacts with a hydrophobic transmembrane domain III (amino acids 210-260 of SEQ ID NO:1 or 2) or domain IV (amino acids 400-450 of SEQ ID NO:1 or 2) of the protein.
49. A method of identifying an agent that modulates the interaction of glucose regulated protein 78 (GRP78) with a cytosolic component that mediates apoptosis, the method comprising:
 - a) providing glucose regulated protein 78 (GRP78) integrally-associated with a membrane;
 - b) providing a cytosolic component comprising at least one caspase;
 - c) providing an agent;
 - d) contacting the protein of a) with the component of b) and the agent of c) simultaneously or in succession; and
 - e) determining the effect of the agent on the interaction of the protein and the component as compared to a control.
50. The method of claim 49, wherein the caspase is caspase-7.
51. The method of claim 49, wherein the glucose regulated protein 78 (GRP78) integrally-associated with a membrane is a microsome complex.
52. The method of claim 49, wherein the effect of the agent is to inhibit the interaction of the protein and the component.
53. The method of claim 49, wherein the assay is performed on a cell.
54. The method of claim 53, further comprising contacting the cell with etoposide.
55. The method of claim 54, wherein the determining is by measuring cell survival in the presence and absence of the agent.
56. A glucose regulated protein (GRP) inhibitory nucleic acid molecule comprising a nucleic acid that interacts with a glucose regulated protein (GRP) polynucleotide.
57. The GRP inhibitory nucleic acid molecule of claim 56, wherein the nucleic acid is an antisense molecule.
58. The antisense molecule of claim 57, wherein the antisense molecule is selected from the group consisting of:

- (a) a nucleic acid comprising a sequence that is at least 80% identical to SEQ ID NO:3 or a fragment and specifically interacts with a GRP polynucleotide;
 - (b) a nucleic acid comprising a sequence that is at least 90% identical to SEQ ID NO:3 or a fragment and specifically interacts with a GRP polynucleotide;
 - (c) a nucleic acid comprising a sequence that is at least 95% identical to SEQ ID NO:3 or a fragment and specifically interacts with a GRP polynucleotide;
 - (d) a nucleic acid comprising a sequence as set forth in SEQ ID NO:3; and
 - (e) a nucleic acid consisting of the sequence as set forth in SEQ ID NO:3.
59. The antisense molecule of claim 56, wherein the GRP polynucleotide is a GRP78 polynucleotide.
60. The GRP inhibitory nucleic acid molecule of claim 56, wherein the nucleic acid is a small inhibitory nucleic acid (siNA) molecule.
61. The GRP inhibitory nucleic acid molecule of claim 60, wherein the siNA molecule is selected from the group consisting of:
- (a) a nucleic acid comprising a sequence that is at least 90% identical to SEQ ID NO:4 and its complement and specifically interacts with a GRP polynucleotide;
 - (b) a nucleic acid comprising a sequence that is at least 95% identical to SEQ ID NO:4 and its complement and specifically interacts with a GRP polynucleotide;
 - (c) a nucleic acid comprising a sequence as set forth in SEQ ID NO:4 and its complement; and
 - (d) a nucleic acid consisting of the sequence set forth in SEQ ID NO:4 and its complement.
62. A glucose regulated protein modulating agent comprising a soluble domain of a GRP protein.
63. A method of identifying an agent that modulates the interaction of glucose regulated protein 78 (GRP78) with a cytosolic component that mediates apoptosis, the method comprising:

- (a) providing a polypeptide comprising the ATP-binding domain of glucose regulated protein 78 (GRP78);
 - (b) providing a cytosolic component comprising at least one caspase;
 - (c) providing an agent;
 - (d) contacting the polypeptide of a) with the component of (e) and the agent of c) simultaneously or in succession; and
 - (f) determining the effect of the agent on the interaction of the polypeptide and the component as compared to a control.
64. The method of claim 63, wherein the polypeptide comprises amino acids 125-275 of SEQ ID NO:2.
65. The method of claim 63, wherein the polypeptide comprises amino acids 150-250 of SEQ ID NO:2.
66. The method of claim 63, wherein the polypeptide comprises amino acids 175-201 of SEQ ID NO:1 or 2.
67. A method of identifying an agent that modulates the interaction of glucose regulated protein 78 (GRP78) with a membrane, the method comprising:
- (a) providing a polypeptide comprising the hydrophobic transmembrane domain III (amino acids 210-260 of SEQ ID NO:1 or 2) and/or domain IV (amino acids 400-450 of SEQ ID NO:1 or 2) of the protein of glucose regulated protein 78 (GRP78);
 - (b) providing an agent;
 - (c) contacting the polypeptide of a) the agent of b) simultaneously or in succession; and
 - (d) determining the effect of the agent on the interaction of the polypeptide with the membrane as compared to a control.
68. A method of modulating apoptosis, the method comprising contacting a cell comprising a caspase polypeptide with an agent that regulates the interaction of the polypeptide with glucose regulated protein 78 (GRP78) endoplasmic reticulum transmembrane protein.
69. The method claim 68, wherein the caspase is selected from the group consisting of Ced-3, caspase-1, caspase-2,

- caspase-4, caspase-5, caspase-6, caspase-7, caspase-8, caspase-9, caspase-10, and caspase 11-14.
70. The method of claim 69, wherein the caspase is caspase-7.
71. The method of claim 68, wherein the modulating is by promoting apoptosis.
72. The method of claim 68, wherein the modulating is by inhibiting apoptosis.
73. The method of claim 68, wherein the agent is a polypeptide.
74. The method of claim 68, wherein the agent is a small molecule.
75. The method of claim 74, wherein the polypeptide is a fragment of the polypeptide consisting of SEQ ID NO:2.
76. The method of claim 75, wherein the fragment comprises a soluble domain of the polypeptide comprising SEQ ID NO:2.
77. The method of claim 68, wherein the agent is a nucleic acid molecule.
78. The method of claim 77, wherein the nucleic acid is an antisense molecule, a ribozyme, a siRNA, or a combination thereof.
79. The method of claim 78, wherein the antisense molecule interacts with a GRP78 polynucleotide.
80. The method of claim 78, wherein the siRNA interacts with a GRP78 polynucleotide.
81. The method of claim 79, wherein the antisense molecule comprises a sequence that is at least 80% identical to SEQ ID NO:3 and specifically interacts with a polynucleotide comprising SEQ ID NO:1.
82. The method of claim 81, wherein the antisense molecule comprises a sequence that is at least 90% identical to SEQ ID NO:3 and specifically interacts with a polynucleotide comprising SEQ ID NO:1.
83. The method of claim 81, wherein the antisense molecule comprises SEQ ID NO:3.
84. The method of claim 81, wherein the antisense molecule consists of SEQ ID NO:3.

85. The method of claim 80, wherein the siRNA comprises a sequence that is about 90% identical to SEQ ID NO:4 and its complement.
86. The method of claim 85, wherein the siRNA comprise a sequence that is about 95% identical to SEQ ID NO:4 and its complement.
87. The method of claim 85, wherein the siRNA comprises SEQ ID NO:4 and its complement.
88. The method of claim 85, wherein the siRNA consists of SEQ ID NO:4 and its complement.
89. The method of claim 68, wherein the method further comprises contacting the cell with a chemotherapeutic agent.
90. A method of modulating apoptosis, the method comprising contacting a cell comprising a glucose regulated protein 94 (GRP94) endoplasmic reticulum transmembrane protein with an agent that regulates the interaction of the transmembrane protein with a cytosolic component that mediates apoptosis.
91. A method of inhibiting apoptosis in a target tissue, the method comprising overexpressing GRP78 or GRP94 in said tissue.
92. The method of claim 91, wherein the tissue is neuronal tissue.
93. The method of claim 91, wherein the tissue is vascular tissue.
94. The method of claim 91, wherein the tissue is cardiac tissue.
95. A method of identifying an agent that modulates the interaction of glucose regulated protein 94 (GRP94) with a cytosolic component that mediates apoptosis, the method comprising:
 - (a) providing glucose regulated protein 94 (GRP94);
 - (b) providing a cytosolic component comprising at least one caspase;
 - (c) providing an agent;
 - (d) contacting the protein of (a) with the component of (b) and the agent of (c) simultaneously or in succession;and

- (e) determining the effect of the agent on the interaction of the protein and the component as compared to a control.
96. A nucleic acid construct comprising a glucose regulated protein (GRP) inhibitory nucleic acid molecule operably linked to an expression control element.
97. The nucleic acid construct of claim 96, wherein the nucleic acid is an antisense molecule.
98. The nucleic acid construct of claim 97, wherein the antisense molecule is selected from the group consisting of:
- (a) a nucleic acid comprising a sequence that is at least 80% identical to SEQ ID NO:3 or a fragment and specifically interacts with a GRP polynucleotide;
 - (b) a nucleic acid comprising a sequence that is at least 90% identical to SEQ ID NO:3 or a fragment and specifically interacts with a GRP polynucleotide;
 - (c) a nucleic acid comprising a sequence that is at least 95% identical to SEQ ID NO:3 or a fragment and specifically interacts with a GRP polynucleotide;
 - (d) a nucleic acid comprising a sequence as set forth in SEQ ID NO:3; and
 - (e) a nucleic acid consisting of the sequence as set forth in SEQ ID NO:3.
99. The nucleic acid construct of claim 96, wherein the inhibitory nucleic acid molecule is a small inhibitory nucleic acid (siNA) molecule.
100. The nucleic acid construct of claim 99, wherein the siNA molecule is selected from the group consisting of:
- (a) a nucleic acid comprising a sequence that is at least 90% identical to SEQ ID NO:4 and its complement and specifically interacts with a GRP polynucleotide;
 - (b) a nucleic acid comprising a sequence that is at least 95% identical to SEQ ID NO:4 and its complement and specifically interacts with a GRP polynucleotide;
 - (c) a nucleic acid comprising a sequence as set forth in SEQ ID NO:4 and its complement; and
 - (d) a nucleic acid consisting of the sequence set forth in SEQ ID NO:4 and its complement.

101. The nucleic acid construct of claim 96, wherein the expression control element comprises a glucose responsive protein 78 (grp78) promoter sequence.
102. The nucleic acid construct of claim 101, wherein the grp78 promoter sequence comprises a sequence from about 3000 base pairs 5' of the site of initiation of transcription of the grp78 coding sequence to 200 base pairs 3' of the site of initiation of the grp78 coding sequence.
103. The nucleic acid construct of claim 99, wherein the siNA molecule disrupts expression of an endogenous GRP polynucleotide.
104. The nucleic acid construct of claim 103, wherein the endogenous GPR polynucleotide is a GRP78 polynucleotide.
105. A recombinant vector comprising the nucleic acid construct of claim 96.
106. The recombinant vector of claim 105, wherein the vector is an animal cell expression vector.
107. The recombinant vector of claim 105, wherein the vector is a viral vector.
108. The recombinant vector of claim 107, wherein the viral vector is selected from the group consisting of retroviral vectors and DNA viral vectors.
109. A pharmaceutical composition comprising the nucleic acid construct of claim 96 in a pharmaceutically acceptable carrier.
110. A method for inhibiting cell proliferation comprising contacting a target cell having a cell proliferative disorder with a nucleic acid construct of claim 96.
111. A method for treating a cell proliferative disorder in a subject comprising administering to the subject a nucleic acid construct of claim 96.
112. The method of claims 111, wherein the subject is a mammal.
113. The method of claim 112, wherein the mammal is a human.
114. The method of claims 111, wherein the administration is by in vivo administration.

115. The method of claim 114, wherein the in vivo administration is by systemic, local, or topical administration.
116. The method of claims 111, wherein the administration is by ex vivo administration.
117. The method of claims 111, wherein the cell proliferative disorder is a neoplastic disorder.
118. The method of claim 117, wherein the neoplastic disorder is selected from the group consisting of lung cancer, colon-rectum cancer, breast cancer, prostate cancer, urinary tract cancer, uterine cancer lymphoma, oral cancer, pancreatic cancer, leukemia, melanoma, stomach cancer, thyroid cancer, liver cancer, and brain cancer and ovarian cancer.
119. A nucleic acid construct comprising a glucose regulated protein (GRP) polynucleotide operably linked to an expression control element.
120. The nucleic acid construct of claim 119, wherein the expression control element comprises a glucose responsive protein 78 (grp78) promoter sequence.
121. The nucleic acid construct of claim 119, wherein the GRP polynucleotide comprises a GRP78 polynucleotide and/or a GRP94 polynucleotide.
122. The nucleic acid construct of claim 121, wherein the GRP polynucleotide is selected from the group consisting of:
 - (a) a polynucleotide comprising a sequence that is at least 80% identical to SEQ ID NO:1, wherein a polypeptide produced from the polynucleotide inhibits apoptosis;
 - (b) a polynucleotide comprising a sequence that is at least 90% identical to SEQ ID NO:1, wherein a polypeptide produced from the polynucleotide inhibits apoptosis;
 - (c) a polynucleotide comprising a sequence that is at least 95% identical to SEQ ID NO:1, wherein a polypeptide produced from the polynucleotide inhibits apoptosis; and
 - (d) a polynucleotide comprising a fragment of SEQ ID NO:1, wherein a polypeptide produced from the polynucleotide inhibits apoptosis.
123. The nucleic acid construct of claim 120, wherein the grp78 promoter sequence comprises a sequence from about 3000 base

pairs 5' of the site of initiation of transcription of the grp78 coding sequence to 200 base pairs 3' of the site of initiation of the grp78 coding sequence.

124. A recombinant vector comprising the nucleic acid construct of claim 119.
125. The recombinant vector of claim 124, wherein the vector is an animal cell expression vector.
126. The recombinant vector of claim 124, wherein the vector is a viral vector.
127. The recombinant vector of claim 126, wherein the viral vector is selected from the group consisting of retroviral vectors and DNA viral vectors.
128. A pharmaceutical composition comprising the nucleic acid construct of claim 119 in a pharmaceutically acceptable carrier.
129. A method for inhibiting tissue damage due to ischemia comprising contacting a target cell having a cell susceptible to ischemia with a nucleic acid construct of claim 119.
130. A method for treating ischemic tissue injury in a subject comprising administering to the subject a nucleic acid construct of claim 119.
131. The method of claims 130, wherein the subject is a mammal.
132. The method of claim 131, wherein the mammal is a human.
133. The method of claims 130, wherein the administration is by in vivo administration.
134. The method of claim 133, wherein the in vivo administration is by systemic, local, or topical administration.
135. The method of claims 130, wherein the administration is by ex vivo administration.

Figure 1

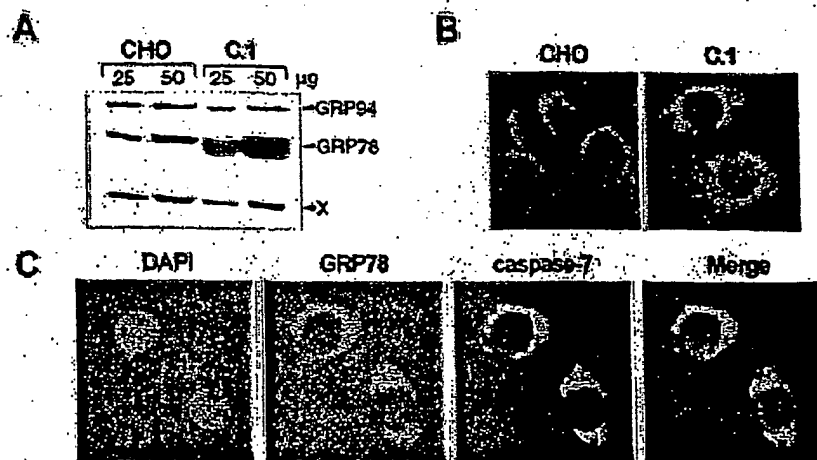


Figure 2

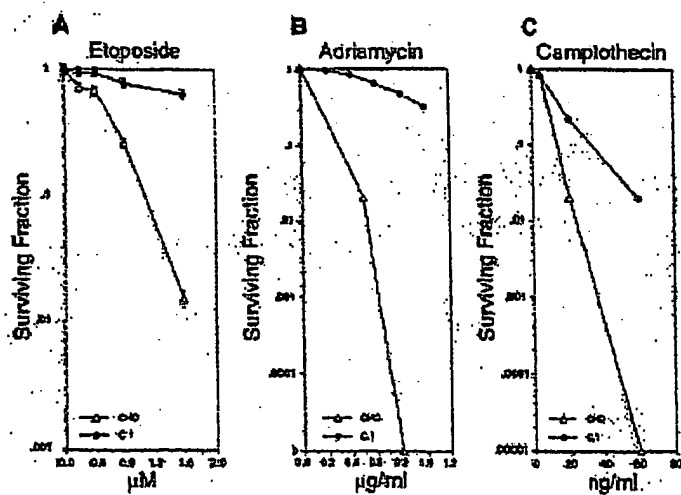


Figure 3

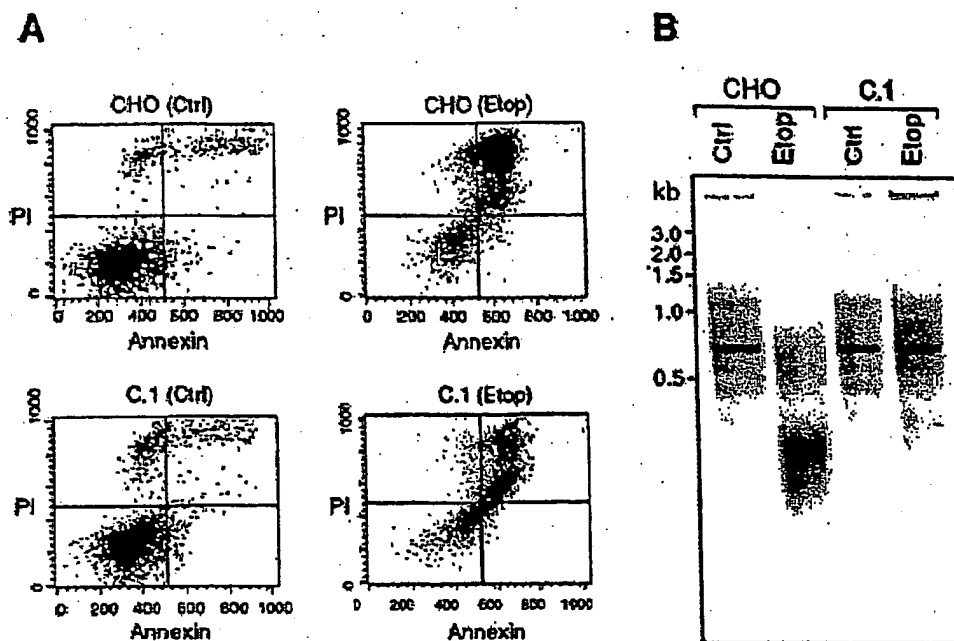


Figure 4

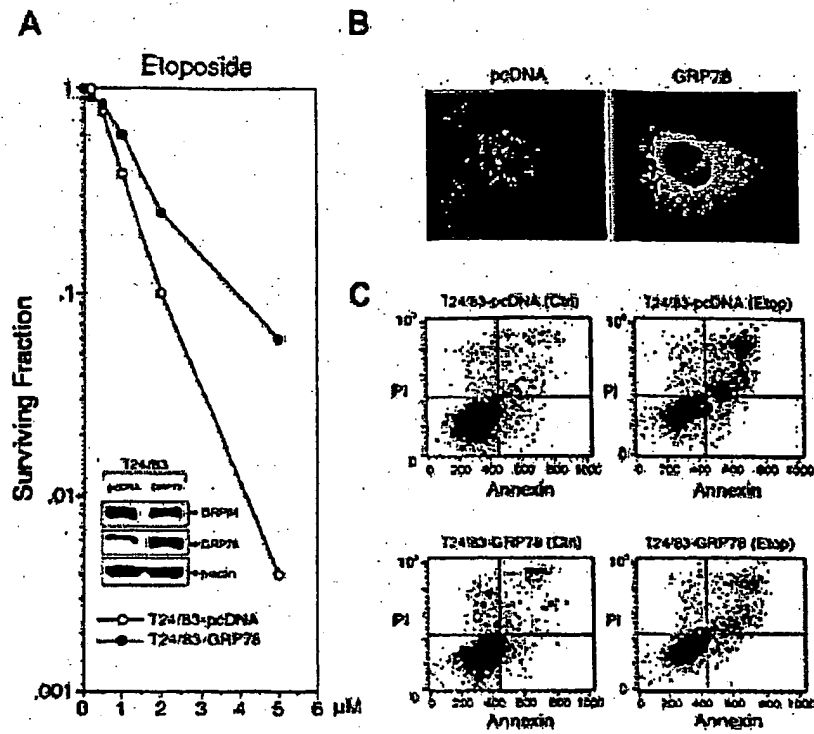


Figure 5

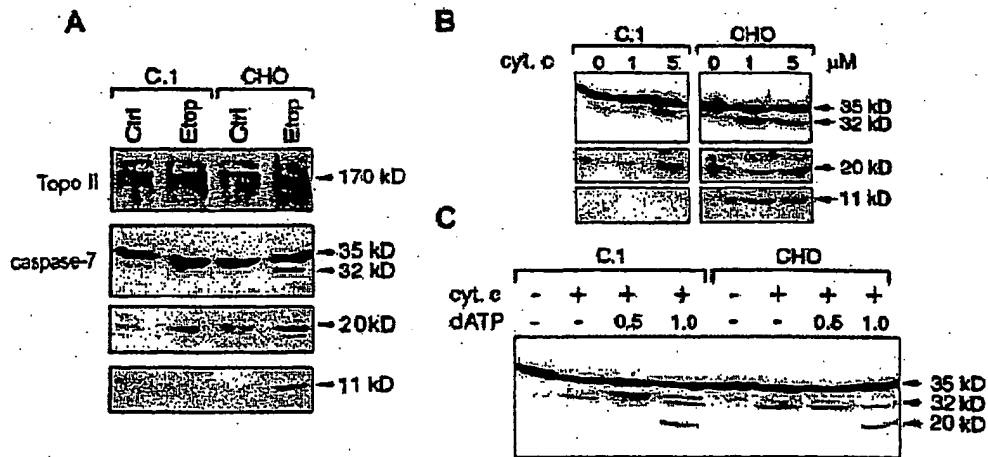


Figure 6

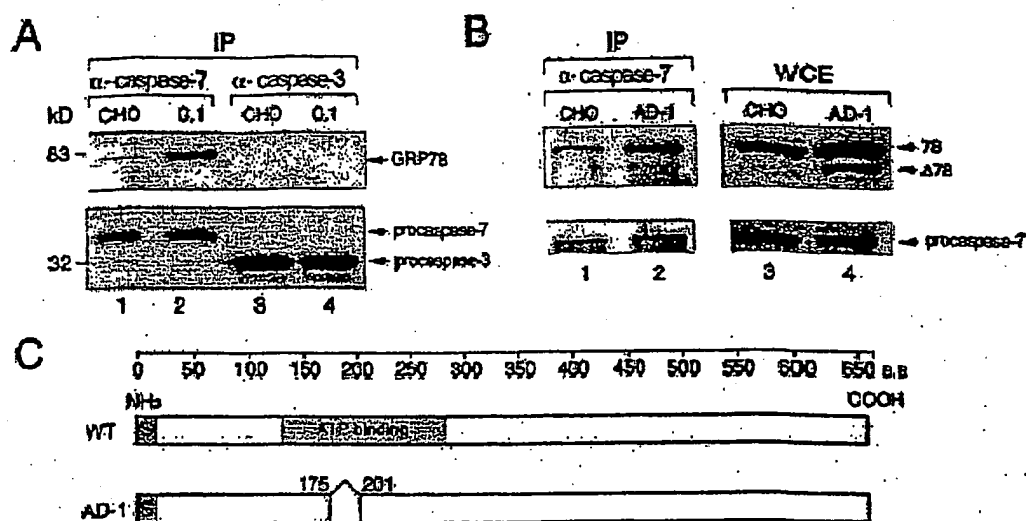


Figure 7

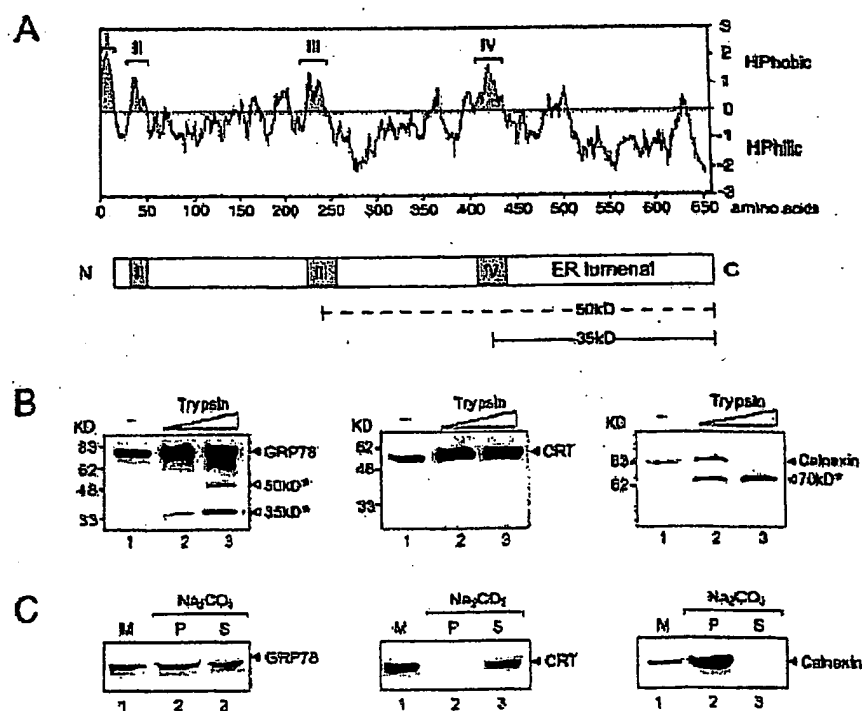


Figure 8

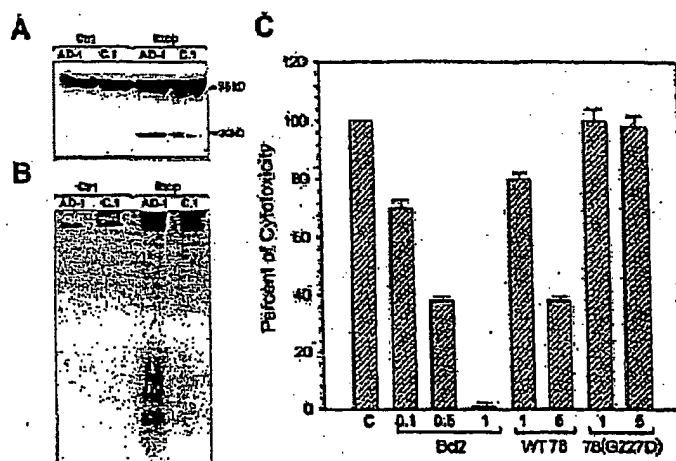
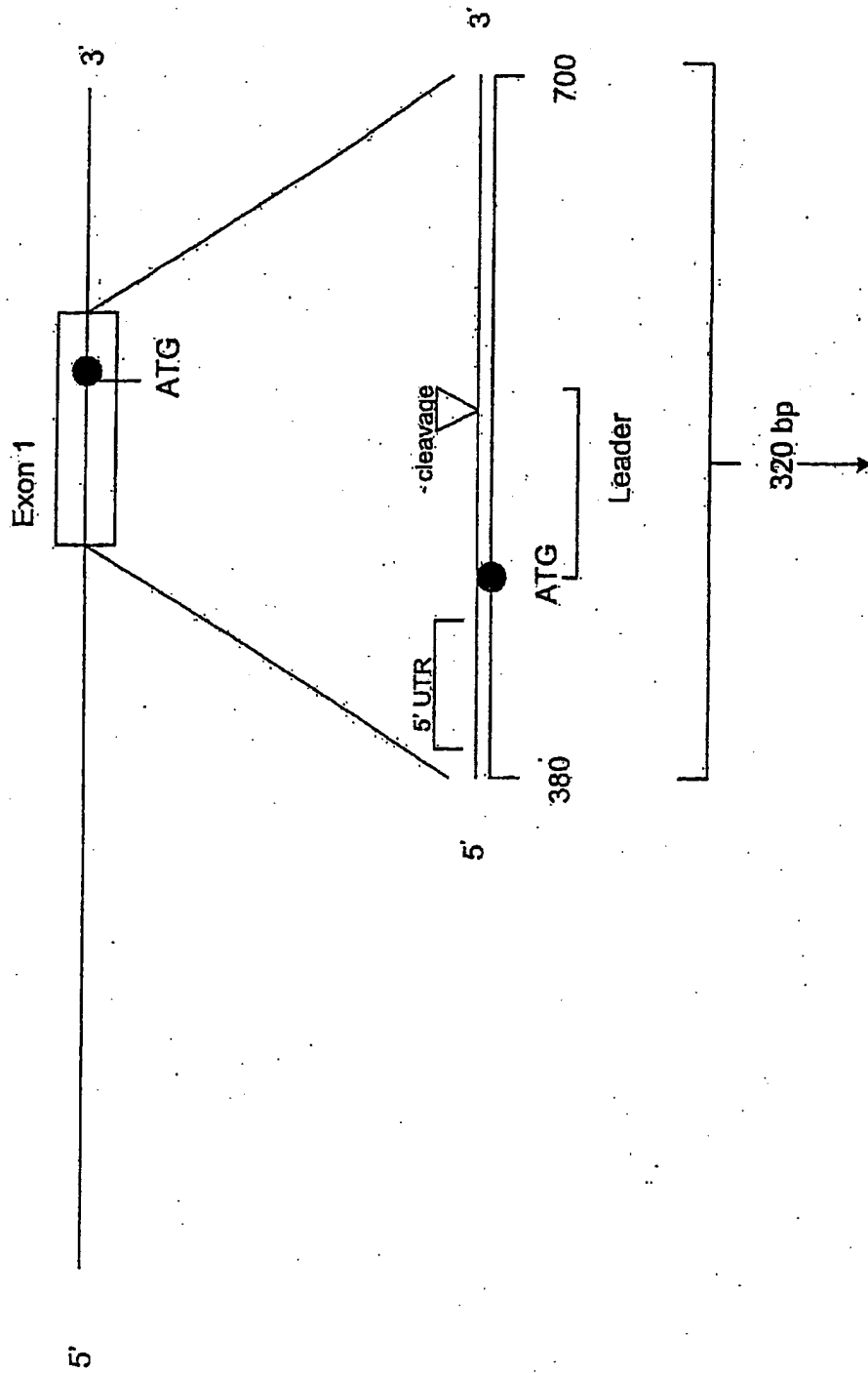


Figure 9

	G ₁	S	G ₂
CHO	40 ± 5	16 ± 3	30 ± 2
CHO + Tuni	62 ± 3	5 ± 1	24 ± 3
CHO + Tg	56 ± 4	9 ± 2	26 ± 2
C1	44 ± 4	20 ± 2	28 ± 5
T24/83-pcDNA	52 ± 7	20 ± 5	30 ± 6
T24/83-pcDNA + Tuni	63 ± 3	3 ± 2	23 ± 2
T24/83-pcDNA + Tg	77 ± 4	6 ± 2	16 ± 2
T24/83-GRP78	60 ± 4	21 ± 9	28 ± 4
T24/83-GRP78 + Tuni	75 ± 8	6 ± 2	22 ± 3
T24/83-GRP78 + Tg	72 ± 4	9 ± 3	22 ± 2

Phu 6.5

Figure 10



Clone into adenovirus vector in reverse orientation

Figure 2. Scheme for subcloning the 320 bp grp78 exon 1 fragment.

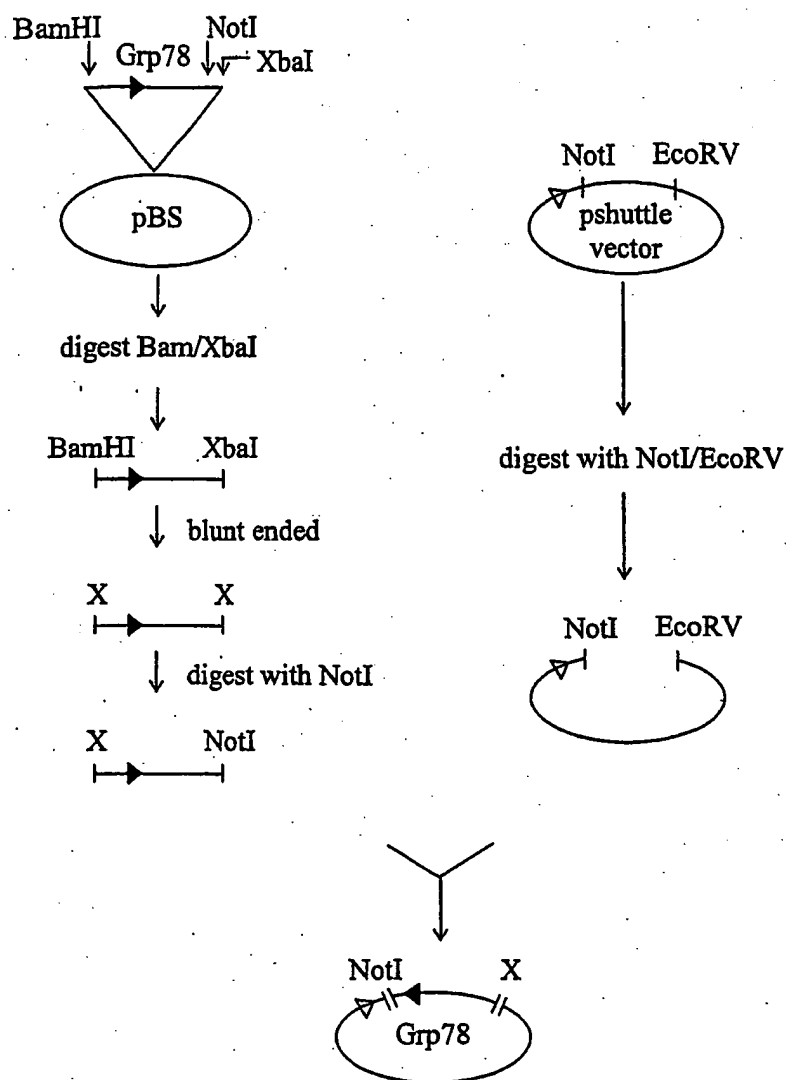


FIG. 11A

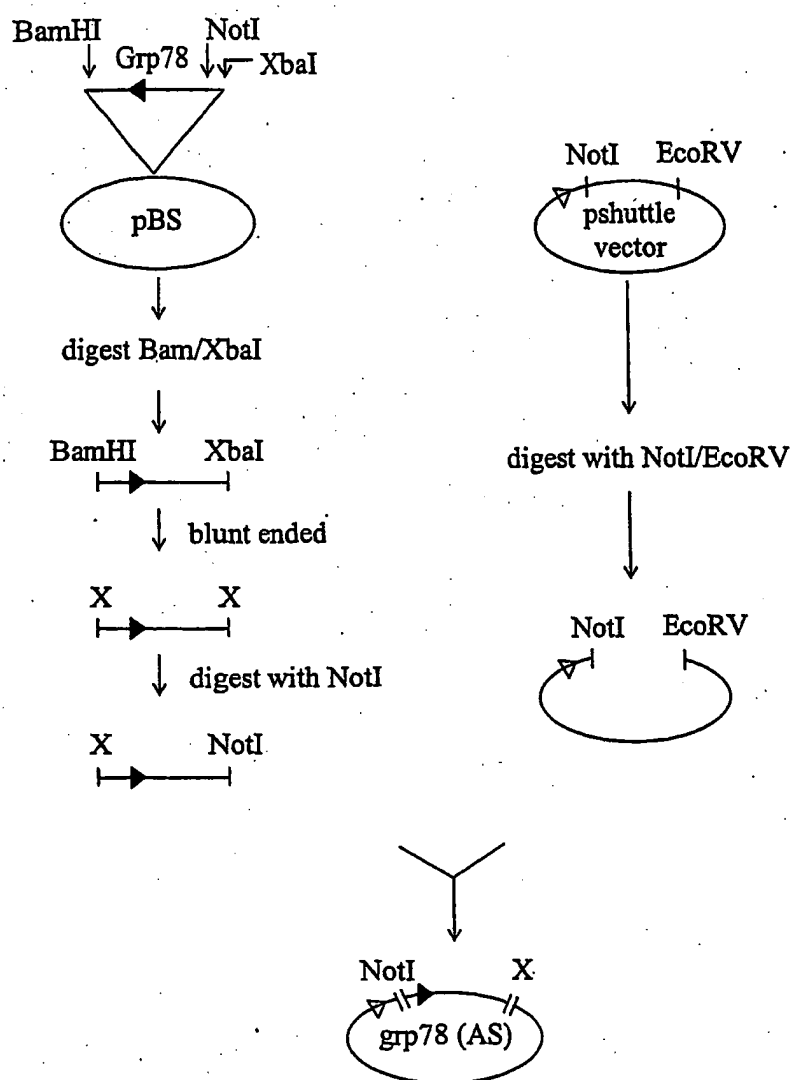


FIG. 11B

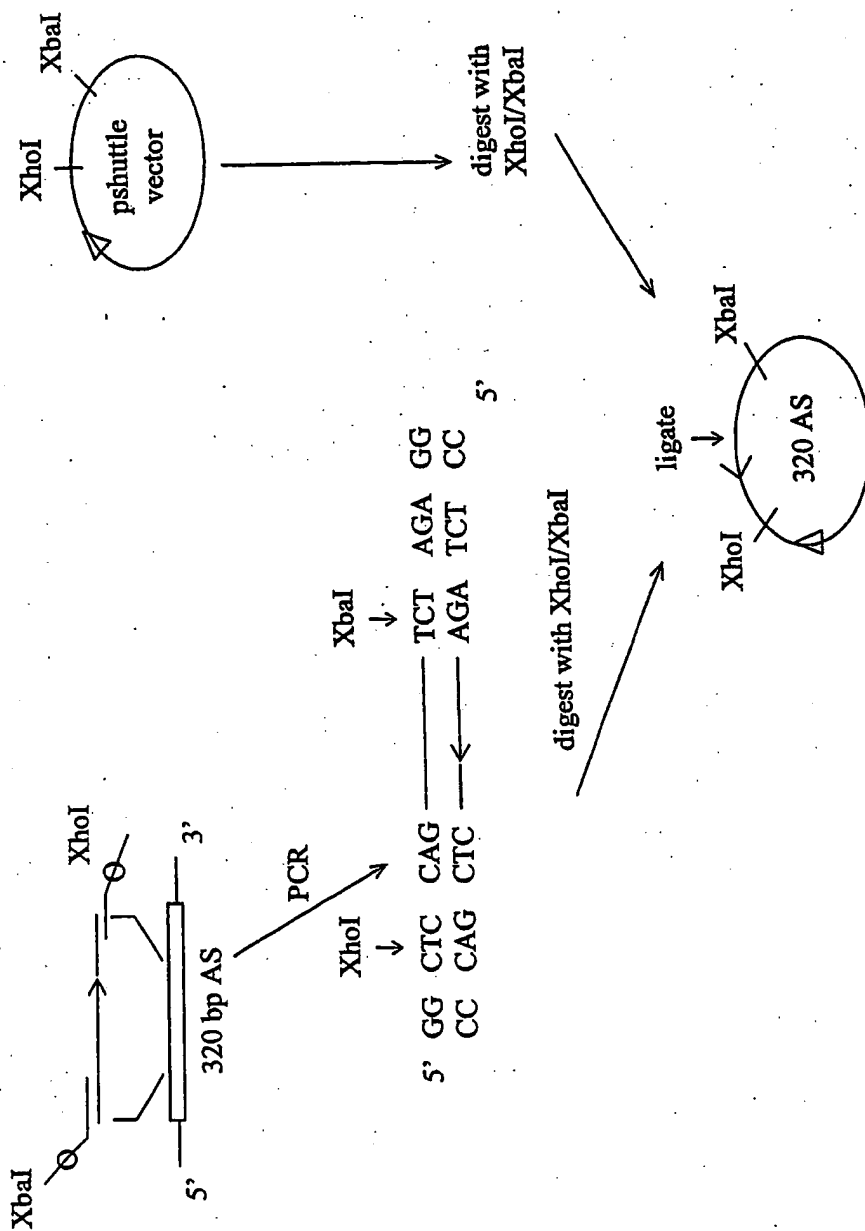


FIG. 11C

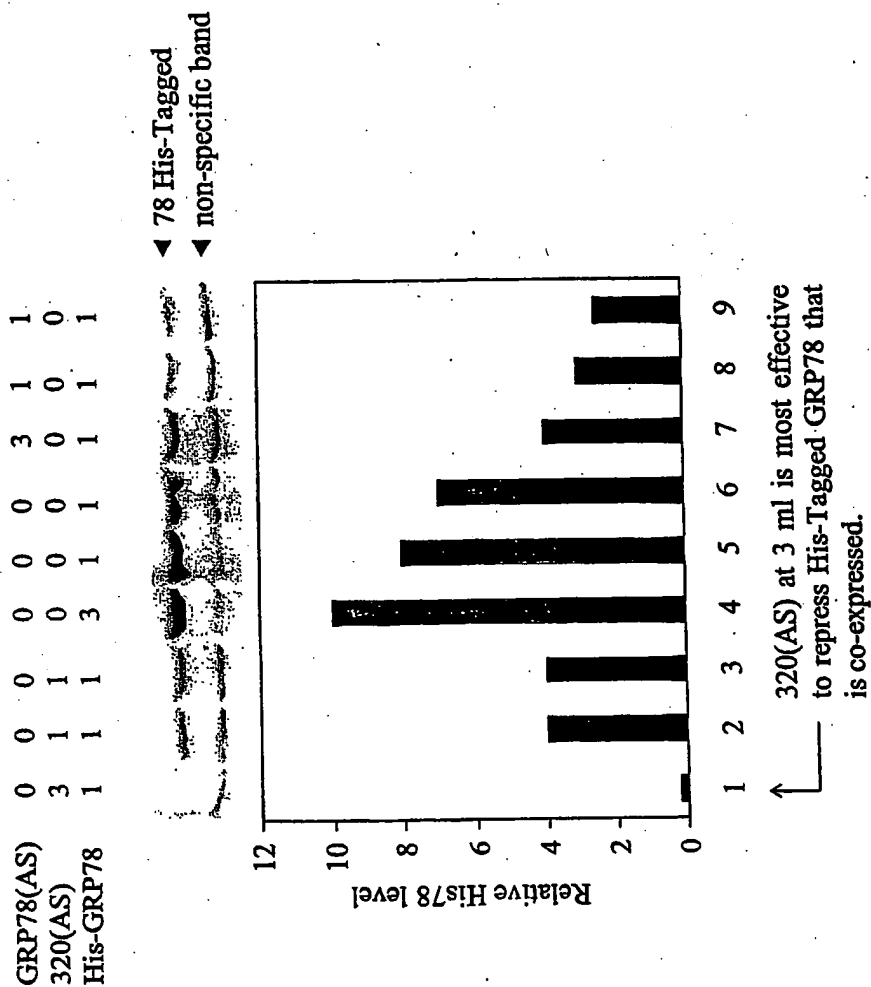


FIG. 12

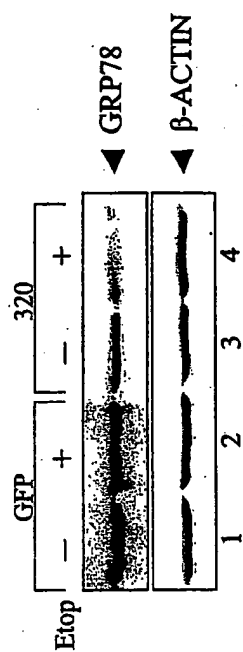


FIG. 13A

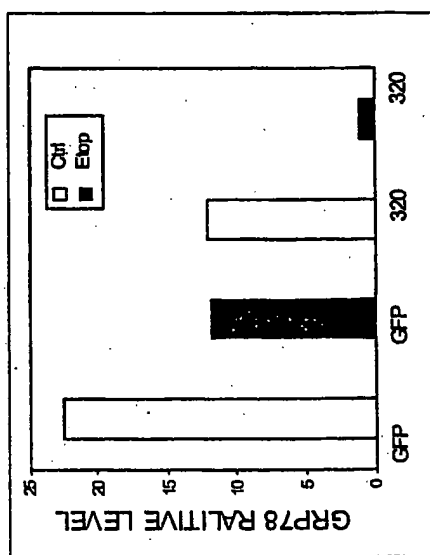


FIG. 13B

TRANSFECTED MDA-MB-435 CELLS: Adenovirus supernatant 0.5 ml/well (6-well dish), 68 hrs
ETOPOSIDE TREATMENT: 20 μ m, 6 hrs, recovered for 4 hrs

FIG. 14

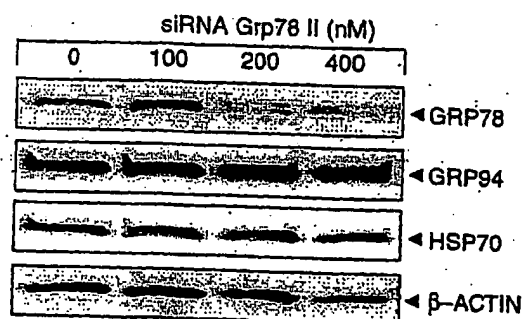
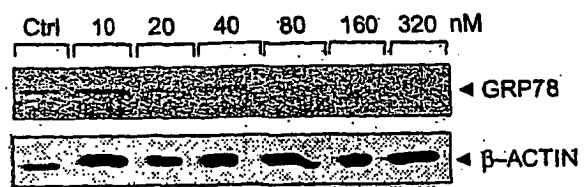


FIG. 15



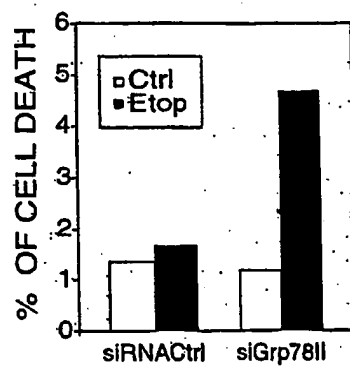


FIG. 16

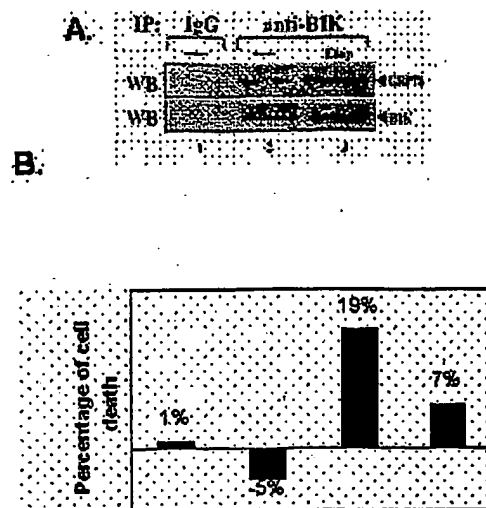


Fig 17A-B

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<120> METHODS AND COMPOSITIONS FOR MODULATING
APOPTOSIS

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ccgcctgcaa gtcggaaatt gcgctgtgct cctgtgtctac ggcctgtggc tggactgcct      180
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                               Met Lys Leu Ser Leu Val Ala Ala Met
                               1               5

```

```

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Leu Leu Leu Leu Ser Ala Ala Arg Ala Glu Glu Glu Asp Lys Lys Glu
  10               15               20               25

```

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              30               35               40

```

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gtc ggc gtg ttc aag aac ggc cgc gtg gag atc atc gcc aac gat cag      375
Val Gly Val Phe Lys Asn Gly Arg Val Glu Ile Ile Ala Asn Asp Gln
      45               50               55

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ggc aac cgc atc acg ccg tcc tat gtc gcc ttc act cct gaa ggg gaa      423
Gly Asn Arg Ile Thr Pro Ser Tyr Val Ala Phe Thr Pro Glu Gly Glu
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```

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Asn Thr Val Phe Asp Ala Lys Arg Leu Ile Gly Arg Thr Trp Asn Asp
      90               95               100               105

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Pro Ser Val Gln Gln Asp Ile Lys Phe Leu Pro Phe Lys Val Val Glu
      110               115               120

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gtt act gta cca gcc tat ttt aat gat gcc caa cgc caa gca acc aaa Val Thr Val Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln Ala Thr Lys 170 175 180 185	759
gac gct gga act att gct ggc cta aat gtt atg agg atc atc aac gag Asp Ala Gly Thr Ile Ala Gly Leu Asn Val Met Arg Ile Ile Asn Glu 190 195 200	807
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Arg Val Glu Ile Ile Ala Asn Asp Gln Gly Asn Arg Ile Thr Pro Ser
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Tyr Val Ala Phe Thr Pro Glu Gly Glu Arg Leu Ile Gly Asp Ala Ala
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Lys Asn Gln Leu Thr Ser Asn Pro Glu Asn Thr Val Phe Asp Ala Lys
 85 90 95
 Arg Leu Ile Gly Arg Thr Trp Asn Asp Pro Ser Val Gln Gln Asp Ile
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 Lys Phe Leu Pro Phe Lys Val Val Glu Lys Lys Thr Lys Pro Tyr Ile
 115 120 125
 Gln Val Asp Ile Gly Gly Gly Gln Thr Lys Thr Phe Ala Pro Glu Glu
 130 135 140
 Ile Ser Ala Met Val Leu Thr Lys Met Lys Glu Thr Ala Glu Ala Tyr
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 Leu Gly Lys Lys Val Thr His Ala Val Val Thr Val Pro Ala Tyr Phe
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 Tyr Gly Leu Asp Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp
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 Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly
 225 230 235 240
 Val Phe Glu Val Val Ala Thr Asn Gly Asp Thr His Leu Gly Gly Glu
 245 250 255
 Asp Phe Asp Gln Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys
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 Ser Thr Met Lys Pro Val Gln Lys Val Leu Glu Asp Ser Asp Leu Lys
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Met Arg Leu Arg Arg Leu Ala Leu

1

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Phe Pro Gly	Val Ala Leu	Leu Leu Ala	Ala Ala Arg	Leu Ala Ala	Ala	

10

15

20

tcc gac gtg	cta gaa ctc	acg gac gac	aac ttc gag	agt cgc atc	tcc	209
Ser Asp Val	Leu Glu Thr	Asp Asp Asn	Phe Glu Ser	Arg Ile Ser		

25

30

35

40

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Asp Thr Gly	Ser Ala Gly	Leu Met Leu	Val Glu Phe	Phe Ala Pro	Trp	

45

50

55

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Arg Leu Lys Gly Ile Val Pro Leu Ala Lys Val Asp Cys Thr Ala Asn			
75	80	85	
act aac acc tgt aat aaa tat gga gtc agt gga tat cca acc ctg aag			401
Thr Asn Thr Cys Asn Lys Tyr Gly Val Ser Gly Tyr Pro Thr Leu Lys			
90	95	100	
ata ttt aga gat ggt gaa gaa gca ggt gct tat gat gga cct agg act			449
Ile Phe Arg Asp Gly Glu Glu Ala Gly Ala Tyr Asp Gly Pro Arg Thr			
105	110	115	120
gct gat gga att gtc agc cac ttg aag aag cag gca gga cca gct tca			497
Ala Asp Gly Ile Val Ser His Leu Lys Lys Gln Ala Gly Pro Ala Ser			
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gtg cct ctc agg act gag gaa gaa ttt aag aaa ttc att agt gat aaa			545
Val Pro Leu Arg Thr Glu Glu Glu Phe Lys Lys Phe Ile Ser Asp Lys			
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gat gcc tct ata gta ggt ttt ttc gat gat tca ttc agt gag gct cac			593
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155	160	165	
tcc gag ttc cta aaa gca gcc agc aac ttg agg gat aac tac cga ttt			641
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Ala His Thr Asn Val Glu Ser Leu Val Asn Glu Tyr Asp Asp Asn Gly			
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Glu Gly Ile Ile Leu Phe Arg Pro Ser His Leu Thr Asn Lys Phe Glu			
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Asp Lys Thr Val Ala Tyr Thr Glu Gln Lys Met Thr Ser Gly Lys Ile			
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Glu Asp Asn Lys Asp Leu Ile Gln Gly Lys Asp Leu Leu Ile Ala Tyr			
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Tyr Asp Val Asp Tyr Glu Lys Asn Ala Lys Gly Ser Asn Tyr Trp Arg			
265	270	275	280
aac agg gta atg atg gtg gca aag aaa ttc ctg gat gct ggg cac aaa			977
Asn Arg Val Met Met Val Ala Lys Lys Phe Leu Asp Ala Gly His Lys			
285	290	295	
ctc aac ttt gct gta gct agc cgc aaa acc ttt agc cat gaa ctt tct			1025
Leu Asn Phe Ala Val Ala Ser Arg Lys Thr Phe Ser His Glu Leu Ser			
300	305	310	

gat ttt ggc ttg gag agc act gct gga gag att cct gtt gtt gct atc Asp Phe Gly Leu Glu Ser Thr Ala Gly Glu Ile Pro Val Val Ala Ile 315 320 325	1073
aga act gct aaa gga gag aag ttt gtc atg cag gag gag ttc tcg cgt Arg Thr Ala Lys Gly Glu Lys Phe Val Met Gln Glu Glu Phe Ser Arg 330 335 340	1121
gat ggg aag gct ctg gag agg ttc ctg cag gat tac ttt gat ggc aat Asp Gly Lys Ala Leu Glu Arg Phe Leu Gln Asp Tyr Phe Asp Gly Asn 345 350 355 360	1169
ctg aag aga tac ctg aag tct gaa cct atc cca gag agc aat gat ggg Leu Lys Arg Tyr Leu Lys Ser Glu Pro Ile Pro Glu Ser Asn Asp Gly 365 370 375	1217
cct gtg aag gta gtg gta gca gag aat ttt gat gaa ata gtg aat aat Pro Val Lys Val Val Val Ala Glu Asn Phe Asp Glu Ile Val Asn Asn 380 385 390	1265
gaa aat aaa gat gtg ctg att gaa ttt tat gcc cct tgg tgt ggt cac Glu Asn Lys Asp Val Leu Ile Glu Phe Tyr Ala Pro Trp Cys Gly His 395 400 405	1313
tgt aag aac ctg gag ccc aag tat aaa gaa ctt ggc gag aag ctc agc Cys Lys Asn Leu Glu Pro Lys Tyr Lys Glu Leu Gly Glu Lys Leu Ser 410 415 420	1361
aaa gac cca aat atc gtc ata gcc aag atg gat gcc aca gcc aat gat Lys Asp Pro Asn Ile Val Ile Ala Lys Met Asp Ala Thr Ala Asn Asp 425 430 435 440	1409
gtg cct tct cca tat gaa gtc aga ggt ttt cct acc ata tac ttc tct Val Pro Ser Pro Tyr Glu Val Arg Gly Phe Pro Thr Ile Tyr Phe Ser 445 450 455	1457
cca gcc aac aag aag cta aat cca aag aaa tat gaa ggt ggc cgt gaa Pro Ala Asn Lys Lys Leu Asn Pro Lys Lys Tyr Glu Gly Gly Arg Glu 460 465 470	1505
tta agt gat ttt att agc tat cta caa aga gaa gct aca aac ccc cct Leu Ser Asp Phe Ile Ser Tyr Leu Gln Arg Glu Ala Thr Asn Pro Pro 475 480 485	1553
gta att caa gaa gaa aaa ccc aag aag aag aag aag gca cag gag gat Val Ile Gln Glu Glu Lys Pro Lys Lys Lys Lys Lys Ala Gln Glu Asp 490 495 500	1601
ctc taaagcagta gccaaacacc actttgtaaa aggactcttc catcagagat Leu 505	1654
gggaaaacca ttggggagga ctaggaccca tatgggaatt attacctctc agggccgaga	1714
ggacagaatg gatataatct gaatcctgtt aaattttctc taaactgttt cttagctgca	1774
ctgttttatgg aaataccagg accagtttat gttgtgtggtt ttgggaaaaa ttatttgtgt	1834
tgggggaaat gttgtggggg tggggttgag ttgggggtat tttctaattt tttttgtaca	1894
tttgaacag tgacaataaa tgagaccct ttaactgtc aaaaaaaaaa aaaaaaaaaa	1954
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	2014
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<210> 6
 <211> 505
 <212> PRT
 <213> Homo sapiens

<400> 6

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      20           25           30
Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met
      35           40           45
Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala
      50           55           60
Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu
      65           70           75           80
Ala Lys Val Asp Cys Thr Ala Asn Thr Asn Thr Cys Asn Lys Tyr Gly
      85           90           95
Val Ser Gly Tyr Pro Thr Leu Lys Ile Phe Arg Asp Gly Glu Glu Ala
      100          105          110
Gly Ala Tyr Asp Gly Pro Arg Thr Ala Asp Gly Ile Val Ser His Leu
      115          120          125
Lys Lys Gln Ala Gly Pro Ala Ser Val Pro Leu Arg Thr Glu Glu Glu
      130          135          140
Phe Lys Lys Phe Ile Ser Asp Lys Asp Ala Ser Ile Val Gly Phe Phe
      145          150          155          160
Asp Asp Ser Phe Ser Glu Ala His Ser Glu Phe Leu Lys Ala Ala Ser
      165          170          175
Asn Leu Arg Asp Asn Tyr Arg Phe Ala His Thr Asn Val Glu Ser Leu
      180          185          190
Val Asn Glu Tyr Asp Asp Asn Gly Glu Gly Ile Ile Leu Phe Arg Pro
      195          200          205
Ser His Leu Thr Asn Lys Phe Glu Asp Lys Thr Val Ala Tyr Thr Glu
      210          215          220
Gln Lys Met Thr Ser Gly Lys Ile Lys Lys Phe Ile Gln Glu Asn Ile
      225          230          235          240
Phe Gly Ile Cys Pro His Met Thr Glu Asp Asn Lys Asp Leu Ile Gln
      245          250          255
Gly Lys Asp Leu Ile Ala Tyr Tyr Asp Val Asp Tyr Glu Lys Asn
      260          265          270
Ala Lys Gly Ser Asn Tyr Trp Arg Asn Arg Val Met Met Val Ala Lys
      275          280          285
Lys Phe Leu Asp Ala Gly His Lys Leu Asn Phe Ala Val Ala Ser Arg
      290          295          300
Lys Thr Phe Ser His Glu Leu Ser Asp Phe Gly Leu Glu Ser Thr Ala
      305          310          315          320
Gly Glu Ile Pro Val Val Ala Ile Arg Thr Ala Lys Gly Glu Lys Phe
      325          330          335
Val Met Gln Glu Glu Phe Ser Arg Asp Gly Lys Ala Leu Glu Arg Phe
      340          345          350
Leu Gln Asp Tyr Phe Asp Gly Asn Leu Lys Arg Tyr Leu Lys Ser Glu
      355          360          365
Pro Ile Pro Glu Ser Asn Asp Gly Pro Val Lys Val Val Val Ala Glu
      370          375          380
Asn Phe Asp Glu Ile Val Asn Asn Glu Asn Lys Asp Val Leu Ile Glu
      385          390          395          400
Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Asn Leu Glu Pro Lys Tyr
      405          410          415
Lys Glu Leu Gly Glu Lys Leu Ser Lys Asp Pro Asn Ile Val Ile Ala
      420          425          430
Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser Pro Tyr Glu Val Arg

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435 440 445
 Gly Phe Pro Thr Ile Tyr Phe Ser Pro Ala Asn Lys Lys Leu Asn Pro
 450 455 460
 Lys Lys Tyr Glu Gly Gly Arg Glu Leu Ser Asp Phe Ile Ser Tyr Leu
 465 470 475 480
 Gln Arg Glu Ala Thr Asn Pro Pro Val Ile Gln Glu Glu Lys Pro Lys
 485 490 495
 Lys Lys Lys Lys Ala Gln Glu Asp Leu
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<210> 7

<211> 1899

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (69)...(1319)

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 ggccccgc atg ctg cta tcc gtg ccg ctg ctg ctc ggc ctc ctc ggc ctg 110
 Met Leu Leu Ser Val Pro Leu Leu Leu Gly Leu Leu Gly Leu
 1 5 10

 gcc gtc gcc gag ccc gcc gtc tac ttc aag gag cag ttt ctg gac gga 158
 Ala Val Ala Glu Pro Ala Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly
 15 20 25 30

 gac ggg tgg act tcc cgc tgg atc gaa tcc aaa cac aag tca gat ttt 206
 Asp Gly Trp Thr Ser Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe
 35 40 45

 ggc aaa ttc gtt ctc agt tcc ggc aag ttc tac ggt gac gag gag aaa 254
 Gly Lys Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Glu Glu Lys
 50 55 60

 gat aaa ggt ttg cag aca agc cag gat gca cgc ttt tat gct ctg tcg 302
 Asp Lys Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser
 65 70 75

 gcc agt ttc gag cct ttc agc aac aaa ggc cag acg ctg gtg gtg cag 350
 Ala Ser Phe Glu Pro Phe Ser Asn Lys Gly Gln Thr Leu Val Val Gln
 80 85 90

 ttc acg gtg aaa cat gag cag aac atc gac tgt ggg ggc ggc tat gtg 398
 Phe Thr Val Lys His Glu Gln Asn Ile Asp Cys Gly Gly Gly Tyr Val
 95 100 105 110

 aag ctg ttt cct aat agt ttg gac cag aca gac atg cac gga gac tca 446
 Lys Leu Phe Pro Asn Ser Leu Asp Gln Thr Asp Met His Gly Asp Ser
 115 120 125

 gaa tac aac atc atg ttt ggt ccc gac atc tgt ggc cct ggc acc aag 494
 Glu Tyr Asn Ile Met Phe Gly Pro Asp Ile Cys Gly Pro Gly Thr Lys
 130 135 140

 aag gtt cat gtc atc ttc aac tac aag ggc aag aac gtg ctg atc aac 542
 Lys Val His Val Ile Phe Asn Tyr Lys Gly Lys Asn Val Leu Ile Asn
 145 150 155

aag gac atc cgt tgc aag gat gat gag ttt aca cac ctg tac aca ctg Lys Asp Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu 160 165 170	590
att gtg cgg cca gac aac acc tat gag gtg aag att gac aac agc cag Ile Val Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln 175 180 185 190	638
gtg gag tcc ggc tcc ttg gaa gac gat tgg gac ttc ctg cca ccc aag Val Glu Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys 195 200 205	686
aag ata aag gat cct gat gct tca aaa ccg gaa gac tgg gat gag cgg Lys Ile Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg 210 215 220	734
gcc aag atc gat gat ccc aca gac tcc aag cct gag gac tgg gac aag Ala Lys Ile Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys 225 230 235	782
ccc gag cat atc cct gac cct gat gct aag aag ccc gag gac tgg gat Pro Glu His Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp 240 245 250	830
gaa gag atg gac gga gag tgg gaa ccc cca gtg att cag aac cct gag Glu Glu Met Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu 255 260 265 270	878
tac aag ggt gag tgg aag ccc cgg cag atc gac aac cca gat tac aag Tyr Lys Gly Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro Asp Tyr Lys 275 280 285	926
ggc act tgg atc cac cca gaa att gac aac ccc gag tat tct ccc gat Gly Thr Trp Ile His Pro Glu Ile Asp Asn Pro Glu Tyr Ser Pro Asp 290 295 300	974
ccc agt atc tat gcc tat gat aac ttt ggc gtg ctg ggc ctg gac ctc Pro Ser Ile Tyr Ala Tyr Asp Asn Phe Gly Val Leu Gly Leu Asp Leu 305 310 315	1022
tgg cag gtc aag tct ggc acc atc ttt gac aac ttc ctc atc acc aac Trp Gln Val Lys Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asn 320 325 330	1070
gat gag gca tac gct gag gag ttt ggc aac gag acg tgg ggc gta aca Asp Glu Ala Tyr Ala Glu Glu Phe Gly Asn Glu Thr Trp Gly Val Thr 335 340 345 350	1118
aag gca gca gag aaa caa atg aag gac aaa cag gac gag gag cag agg Lys Ala Ala Glu Lys Gln Met Lys Asp Lys Gln Asp Glu Glu Gln Arg 355 360 365	1166
ctt aag gag gag gaa gaa gac aag aaa cgc aaa gag gag gag gag gca Leu Lys Glu Glu Glu Glu Asp Lys Lys Arg Lys Glu Glu Glu Glu Ala 370 375 380	1214
gag gac aag gag gat gat gag gac aaa gat gag gat gag gag gat gag Glu Asp Lys Glu Asp Asp Glu Asp Lys Asp Glu Asp Glu Asp Glu 385 390 395	1262
gag gac aag gag gaa gat gag gag gaa gat gtc ccc ggc cag gcc aag	1310

Glu Asp Lys Glu Glu Asp Glu Glu Glu Asp Val Pro Gly Gln Ala Lys
 400 405 410

gac gag ctg tagagaggcc tgcctccagg gctggactga ggcctgagcg 1359
 Asp Glu Leu
 415

ctcctgccc agagcttgcc gcgccaata atgtctctgt gagactcgag aactttcatt 1419
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 ccccacccc tcccgcctt tttttttttt ttttttaaac tggatattta tcctttgatt 1539
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<210> 8

<211> 417

<212> PRT

<213> Homo sapiens

<400> 8

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 20 25 30
 Trp Thr Ser Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
 35 40 45
 Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Glu Leu Lys Asp Lys
 50 55 60
 Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Ser
 65 70 75 80
 Phe Glu Pro Phe Ser Asn Lys Gly Gln Thr Leu Val Val Gln Phe Thr
 85 90 95
 Val Lys His Glu Gln Asn Ile Asp Cys Gly Gly Gly Tyr Val Lys Leu
 100 105 110
 Phe Pro Asn Ser Leu Asp Gln Thr Asp Met His Gly Asp Ser Glu Tyr
 115 120 125
 Asn Ile Met Phe Gly Pro Asp Ile Cys Gly Pro Gly Thr Lys Lys Val
 130 135 140
 His Val Ile Phe Asn Tyr Lys Gly Lys Asn Val Leu Ile Asn Lys Asp
 145 150 155 160
 Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val
 165 170 175
 Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln Val Glu
 180 185 190
 Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile
 195 200 205
 Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys
 210 215 220
 Ile Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys Pro Glu
 225 230 235 240
 His Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu
 245 250 255
 Met Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys
 260 265 270
 Gly Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro Asp Tyr Lys Gly Thr
 275 280 285
 Trp Ile His Pro Glu Ile Asp Asn Pro Glu Tyr Ser Pro Asp Pro Ser
 290 295 300

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Ile Tyr Ala Tyr Asp Asn Phe Gly Val Leu Gly Leu Asp Leu Trp Gln
305          310          315          320
Val Lys Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu
          325          330          335
Ala Tyr Ala Glu Glu Phe Gly Asn Glu Thr Trp Gly Val Thr Lys Ala
          340          345          350
Ala Glu Lys Lys Gln Met Lys Asp Lys Glu Asp Glu Glu Gln Arg Leu Lys
          355          360          365
Glu Glu Glu Glu Asp Lys Lys Arg Lys Glu Glu Glu Glu Ala Glu Asp
          370          375          380
Lys Glu Asp Asp Glu Asp Lys Asp Glu Asp Glu Glu Asp Glu Glu Asp
385          390          395          400
Lys Glu Glu Asp Glu Glu Glu Asp Val Pro Gly Gln Ala Lys Asp Glu
          405          410          415
Leu

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<210> 9

<211> 1288

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (64)...(1215)

<400> 9

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    Met Ala Arg Ala Leu Val Gln Phe Trp Ala Ile Cys Met Leu Arg
      1          5          10          15

gtg gcg ctg gct acc gtc tat ttc caa gag gaa ttt cta gac gga gag      156
Val Ala Leu Ala Thr Val Tyr Phe Gln Glu Glu Phe Leu Asp Gly Glu
          20          25          30

cat tgg aga aac cga tgg ttg cag tcc acc aat gac tcc cga ttt ggg      204
His Trp Arg Asn Arg Trp Leu Gln Ser Thr Asn Asp Ser Arg Phe Gly
          35          40          45

cat ttt aga ctt tcg tcg ggc aag ttt tat ggt cat aaa gag aaa gat      252
His Phe Arg Leu Ser Ser Gly Lys Phe Tyr Gly His Lys Glu Lys Asp
          50          55          60

aaa ggt ctg caa acc act cag aat ggc cga ttc tat gcc atc tct gca      300
Lys Gly Leu Gln Thr Thr Gln Asn Gly Arg Phe Tyr Ala Ile Ser Ala
          65          70          75

cgc ttc aaa ccg ttc agc aat aaa ggg aaa act ctg gtt att cag tac      348
Arg Phe Lys Pro Phe Ser Asn Lys Gly Lys Thr Leu Val Ile Gln Tyr
          80          85          90          95

aca gta aaa cat gag cag aag atg gac tgt gga ggg ggc tac att aag      396
Thr Val Lys His Glu Gln Lys Met Asp Cys Gly Gly Gly Tyr Ile Lys
          100          105          110

gtc ttt cct gca gac att gac cag aag aac ctg aat gga aaa tcg caa      444
Val Phe Pro Ala Asp Ile Asp Gln Lys Asn Leu Asn Gly Lys Ser Gln
          115          120          125

tac tat att atg ttt gga ccc gat att tgt gga ttt gat atc aag aaa      492

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Tyr Tyr Ile Met Phe Gly Pro Asp Ile Cys Gly Phe Asp Ile Lys Lys	
130 135 140	
ggt cat ggt att tta cat ttc aag aat aag tat cac gaa aac aag aaa	540
Val His Val Ile Leu His Phe Lys Asn Lys Tyr His Glu Asn Lys Lys	
145 150 155	
ctg atc agg tgt aag gtt gat ggc ttc aca cac ctg tac act cta att	588
Leu Ile Arg Cys Lys Val Asp Gly Phe Thr His Leu Tyr Thr Leu Ile	
160 165 170 175	
tta aga cca gat ctt tct tat gat gtg aaa att gat ggt cag tca att	636
Leu Arg Pro Asp Leu Ser Tyr Asp Val Lys Ile Asp Gly Gln Ser Ile	
180 185 190	
gaa tcc ggc agc ata gag tac gac tgg aac tta aca tca ctc aag aag	684
Glu Ser Gly Ser Ile Glu Tyr Asp Trp Asn Leu Thr Ser Leu Lys Lys	
195 200 205	
gaa acg tcc ccg gca gaa tcg aag gat tgg gaa cag act aaa gac aac	732
Glu Thr Ser Pro Ala Glu Ser Lys Asp Trp Glu Gln Thr Lys Asp Asn	
210 215 220	
aaa gcc cag gac tgg gag aag cat ttt ctg gac gcc agc acc agc aag	780
Lys Ala Gln Asp Trp Glu Lys His Phe Leu Asp Ala Ser Thr Ser Lys	
225 230 235	
cag agc gac tgg aac ggt gac ctg gat ggg gac tgg cca gcg ccg atg	828
Gln Ser Asp Trp Asn Gly Asp Leu Asp Gly Asp Trp Pro Ala Pro Met	
240 245 250 255	
ctc cag aag ccc ccg tac cag gat ggc ctg aaa cca gaa ggt att cat	876
Leu Gln Lys Pro Pro Tyr Gln Asp Gly Leu Lys Pro Glu Gly Ile His	
260 265 270	
aaa gac gtc tgg ctc cac cgt aag atg aag aat acc gac tat ttg acg	924
Lys Asp Val Trp Leu His Arg Lys Met Lys Asn Thr Asp Tyr Leu Thr	
275 280 285	
cag tat gac ctc tca gaa ttt gag aac att ggt gcc att ggc ctg gag	972
Gln Tyr Asp Leu Ser Glu Phe Glu Asn Ile Gly Ala Ile Gly Leu Glu	
290 295 300	
ctt tgg cag gtg aga tct gga acc att ttt gat aac ttt ctg atc aca	1020
Leu Trp Gln Val Arg Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr	
305 310 315	
gat gat gaa gag tat gca gat aat ttt ggc aag gcc acc tgg ggc gaa	1068
Asp Asp Glu Glu Tyr Ala Asp Asn Phe Gly Lys Ala Thr Trp Gly Glu	
320 325 330 335	
acc aag ggt cca gaa agg gag atg gat gcc ata cag gcc aag gag gaa	1116
Thr Lys Gly Pro Glu Arg Glu Met Asp Ala Ile Gln Ala Lys Glu Glu	
340 345 350	
atg aag aag gcc cgc gag gaa gag gag gaa gag ctg ctg tcg gga aaa	1164
Met Lys Lys Ala Arg Glu Glu Glu Glu Glu Glu Leu Leu Ser Gly Lys	
355 360 365	
att aac agg cac gaa cat tac ttc aat caa ttt cac aga agg aat gaa	1212
Ile Asn Arg His Glu His Tyr Phe Asn Gln Phe His Arg Arg Asn Glu	

370

375

380

ctt tagtgatccc cattggatat aaggatgact ggtaaaatct cattgctact
Leu

1265

ttaatctaaa aaaaaaaaaa aaa

1288

<210> 10

<211> 384

<212> PRT

<213> Homo sapiens

<400> 10

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			20					25					30		
Trp	Arg	Asn	Arg	Trp	Leu	Gln	Ser	Thr	Asn	Asp	Ser	Arg	Phe	Gly	His
		35					40					45			
Phe	Arg	Leu	Ser	Ser	Gly	Lys	Phe	Tyr	Gly	His	Lys	Glu	Lys	Asp	Lys
		50				55					60				
Gly	Leu	Gln	Thr	Thr	Gln	Asn	Gly	Arg	Phe	Tyr	Ala	Ile	Ser	Ala	Arg
65					70					75				80	
Phe	Lys	Pro	Phe	Ser	Asn	Lys	Gly	Lys	Thr	Leu	Val	Ile	Gln	Tyr	Thr
				85					90					95	
Val	Lys	His	Glu	Gln	Lys	Met	Asp	Cys	Gly	Gly	Gly	Tyr	Ile	Lys	Val
			100					105					110		
Phe	Pro	Ala	Asp	Ile	Asp	Gln	Lys	Asn	Leu	Asn	Gly	Lys	Ser	Gln	Tyr
		115					120					125			
Tyr	Ile	Met	Phe	Gly	Pro	Asp	Ile	Cys	Gly	Phe	Asp	Ile	Lys	Lys	Val
130						135					140				
His	Val	Ile	Leu	His	Phe	Lys	Asn	Lys	Tyr	His	Glu	Asn	Lys	Lys	Leu
145					150					155					160
Ile	Arg	Cys	Lys	Val	Asp	Gly	Phe	Thr	His	Leu	Tyr	Thr	Leu	Ile	Leu
				165					170					175	
Arg	Pro	Asp	Leu	Ser	Tyr	Asp	Val	Lys	Ile	Asp	Gly	Gln	Ser	Ile	Glu
			180					185					190		
Ser	Gly	Ser	Ile	Glu	Tyr	Asp	Trp	Asn	Leu	Thr	Ser	Leu	Lys	Lys	Glu
		195					200					205			
Thr	Ser	Pro	Ala	Glu	Ser	Lys	Asp	Trp	Glu	Gln	Thr	Lys	Asp	Asn	Lys
		210					215					220			
Ala	Gln	Asp	Trp	Glu	Lys	His	Phe	Leu	Asp	Ala	Ser	Thr	Ser	Lys	Gln
225					230					235					240
Ser	Asp	Trp	Asn	Gly	Asp	Leu	Asp	Gly	Asp	Trp	Pro	Ala	Pro	Met	Leu
			245						250					255	
Gln	Lys	Pro	Pro	Tyr	Gln	Asp	Gly	Leu	Lys	Pro	Glu	Gly	Ile	His	Lys
			260					265					270		
Asp	Val	Trp	Leu	His	Arg	Lys	Met	Lys	Asn	Thr	Asp	Tyr	Leu	Thr	Gln
		275					280					285			
Tyr	Asp	Leu	Ser	Glu	Phe	Glu	Asn	Ile	Gly	Ala	Ile	Gly	Leu	Glu	Leu
290						295					300				
Trp	Gln	Val	Arg	Ser	Gly	Thr	Ile	Phe	Asp	Asn	Phe	Leu	Ile	Thr	Asp
305					310					315					320
Asp	Glu	Glu	Tyr	Ala	Asp	Asn	Phe	Gly	Lys	Ala	Thr	Trp	Gly	Glu	Thr
				325					330					335	
Lys	Gly	Pro	Glu	Arg	Glu	Met	Asp	Ala	Ile	Gln	Ala	Lys	Glu	Glu	Met
			340					345					350		
Lys	Lys	Ala	Arg	Glu	Glu	Glu	Glu	Glu	Glu	Leu	Leu	Ser	Gly	Lys	Ile
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Asn	Arg	His	Glu	His	Tyr	Phe	Asn	Gln	Phe	His	Arg	Arg	Asn	Glu	Leu

370 375 380

<210> 11
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (28)...(1560)

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 1 5

cag gga gcg agg agc ccc tcg gag gag cct cca gag gag gaa atc ccc 102
 Gln Gly Ala Arg Ser Pro Ser Glu Glu Pro Pro Glu Glu Glu Ile Pro
 10 15 20 25

aag gag gat ggg atc ttg gtg ctg agc cgc cac acc ctg ggc ctg gcc 150
 Lys Glu Asp Gly Ile Leu Val Leu Ser Arg His Thr Leu Gly Leu Ala
 30 35 40

ctg cgg gag cac cct gcc ctg ctg gtg gaa ttc tat gcc ccg tgg tgt 198
 Leu Arg Glu His Pro Ala Leu Leu Val Glu Phe Tyr Ala Pro Trp Cys
 45 50 55

ggg cac tgc cag gcc ctg gcc ccc gag tac agc aag gca gct gcc gtg 246
 Gly His Cys Gln Ala Leu Ala Pro Glu Tyr Ser Lys Ala Ala Ala Val
 60 65 70

ctc gcg gcc gag tca atg gtg gtc acg ctg gcc aag gtg gat ggg ccc 294
 Leu Ala Ala Glu Ser Met Val Val Thr Leu Ala Lys Val Asp Gly Pro
 75 80 85

gcg cag cgc gag ctg gct gag gag ttt ggt gtg acg gag tac cct acg 342
 Ala Gln Arg Glu Leu Ala Glu Glu Phe Gly Val Thr Glu Tyr Pro Thr
 90 95 100 105

ctc aag ttc ttc cgc aat ggg aac cgc acg cac ccc gag gag tac aca 390
 Leu Lys Phe Phe Arg Asn Gly Asn Arg Thr His Pro Glu Glu Tyr Thr
 110 115 120

gga cca cgg gac gct gag ggc att gcc gag tgg ctg cga cgg cgg gtg 438
 Gly Pro Arg Asp Ala Glu Gly Ile Ala Glu Trp Leu Arg Arg Arg Val
 125 130 135

ggg ccc agt gcc atg cgg ctg gag gat gag gcg gcc gcc cag gcg ctg 486
 Gly Pro Ser Ala Met Arg Leu Glu Asp Glu Ala Ala Ala Gln Ala Leu
 140 145 150

atc ggt ggc cgg gac cta gtg gtc att ggc ttc ttc cag gac ctg cag 534
 Ile Gly Gly Arg Asp Leu Val Val Ile Gly Phe Phe Gln Asp Leu Gln
 155 160 165

gac gag gac gtg gcc acc ttc ttg gcc ttg gcc cag gac gcc ctg gac 582
 Asp Glu Asp Val Ala Thr Phe Leu Ala Leu Ala Gln Asp Ala Leu Asp
 170 175 180 185

atg acc ttt ggc ctc aca gac cgg ccg cgg ctc ttt cag cag ttt ggc 630

Met	Thr	Phe	Gly	Leu	Thr	Asp	Arg	Pro	Arg	Leu	Phe	Gln	Gln	Phe	Gly	
				190					195					200		
ctc	acc	aag	gac	act	gtg	gtt	ctc	ttc	aag	aag	ttt	gat	gag	ggg	cgg	678
Leu	Thr	Lys	Asp	Thr	Val	Val	Leu	Phe	Lys	Lys	Phe	Asp	Glu	Gly	Arg	
			205					210					215			
gca	gac	ttc	ccc	gtg	gac	gag	gag	ctt	ggc	ctg	gac	ctg	ggg	gat	ctg	726
Ala	Asp	Phe	Pro	Val	Asp	Glu	Glu	Leu	Gly	Leu	Asp	Leu	Gly	Asp	Leu	
			220				225					230				
tcg	cgc	ttc	ctg	gtc	aca	cac	agc	atg	cgc	ctg	gtc	acg	gag	ttc	aac	774
Ser	Arg	Phe	Leu	Val	Thr	His	Ser	Met	Arg	Leu	Val	Thr	Glu	Phe	Asn	
			235				240				245					
agc	cag	acg	tct	gcc	aag	atc	ttc	gcg	gcc	agg	atc	ctc	aac	cac	ctg	822
Ser	Gln	Thr	Ser	Ala	Lys	Ile	Phe	Ala	Ala	Arg	Ile	Leu	Asn	His	Leu	
			250		255					260					265	
ctg	ctg	ttt	gtc	aac	cag	acg	ctg	gct	gcg	cac	cgg	gag	ctc	cta	gcg	870
Leu	Leu	Phe	Val	Asn	Gln	Thr	Leu	Ala	Ala	His	Arg	Glu	Leu	Leu	Ala	
				270					275					280		
ggc	ttt	ggg	gag	gca	gct	ccc	cgc	ttc	cgg	ggg	cag	gtg	ctg	ttc	gtg	918
Gly	Phe	Gly	Glu	Ala	Ala	Pro	Arg	Phe	Arg	Gly	Gln	Val	Leu	Phe	Val	
			285					290					295			
gtg	gtg	gac	gtg	gcg	gcc	gac	aat	gag	cac	gtg	ctg	cag	tac	ttt	gga	966
Val	Val	Asp	Val	Ala	Ala	Asp	Asn	Glu	His	Val	Leu	Gln	Tyr	Phe	Gly	
			300				305					310				
ctc	aag	gct	gag	gca	gcc	ccc	act	ctg	cgc	ttg	gtc	aac	ctt	gaa	acc	1014
Leu	Lys	Ala	Glu	Ala	Ala	Pro	Thr	Leu	Arg	Leu	Val	Asn	Leu	Glu	Thr	
			315				320				325					
act	aag	aag	tat	gcg	cct	gtg	gat	ggg	ggc	cct	gtc	acc	gca	gcg	tcc	1062
Thr	Lys	Lys	Tyr	Ala	Pro	Val	Asp	Gly	Gly	Pro	Val	Thr	Ala	Ala	Ser	
			330		335					340					345	
atc	act	gct	ttc	tgc	cat	gca	gtc	ctc	aac	ggc	caa	gtc	aag	ccc	tat	1110
Ile	Thr	Ala	Phe	Cys	His	Ala	Val	Leu	Asn	Gly	Gln	Val	Lys	Pro	Tyr	
				350					355					360		
ctc	ctg	agc	cag	gag	ata	ccc	cct	gat	tgg	gat	cag	cgg	cca	gtt	aag	1158
Leu	Leu	Ser	Gln	Glu	Ile	Pro	Pro	Asp	Trp	Asp	Gln	Arg	Pro	Val	Lys	
			365					370					375			
acc	ctc	gtg	ggc	aag	aat	ttt	gag	cag	gtg	gct	ttt	gac	gaa	acc	aag	1206
Thr	Leu	Val	Gly	Lys	Asn	Phe	Glu	Gln	Val	Ala	Phe	Asp	Glu	Thr	Lys	
			380				385					390				
aat	gtg	ttt	gtc	aag	ttc	tat	gcc	ccg	tgg	tgc	acc	cac	tgc	aag	gag	1254
Asn	Val	Phe	Val	Lys	Phe	Tyr	Ala	Pro	Trp	Cys	Thr	His	Cys	Lys	Glu	
			395			400				405						
atg	gcc	cct	gcc	tgg	gag	gca	ttg	gct	gag	aag	tac	caa	gac	cac	gag	1302
Met	Ala	Pro	Ala	Trp	Glu	Ala	Leu	Ala	Glu	Lys	Tyr	Gln	Asp	His	Glu	
			410		415				420						425	
gac	atc	atc	att	gct	gag	ctg	gat	gcc	acg	gcc	aac	gag	ctg	gat	gcc	1350
Asp	Ile	Ile	Ile	Ala	Glu	Leu	Asp	Ala	Thr	Ala	Asn	Glu	Leu	Asp	Ala	

430 435 440

ttc gct gtg cac ggc ttc cct act ctc aag tac ttc cca gca ggg cca 1398
Phe Ala Val His Gly Phe Pro Thr Leu Lys Tyr Phe Pro Ala Gly Pro
445 450 455

ggg cgg aag gtg att gaa tac aaa agc acc agg gac ctg gag act ttc 1446
Gly Arg Lys Val Ile Glu Tyr Lys Ser Thr Arg Asp Leu Glu Thr Phe
460 465 470

tcc aag ttc ctg gac aac ggg ggc gtg ctg ccc acg gag gag tcc ccg 1494
Ser Lys Phe Leu Asp Asn Gly Gly Val Leu Pro Thr Glu Glu Ser Pro
475 480 485

gag gag cca gca gcc ccg ttc ccg gag cca ccg gcc aac tcc act atg 1542
Glu Glu Pro Ala Ala Pro Phe Pro Glu Pro Pro Ala Asn Ser Thr Met
490 495 500 505

ggg tcc aag gag gaa ctg tagctgcccc cgtgtcaccc ccgccatcac 1590
Gly Ser Lys Glu Glu Leu
510

tgctggacag gagccacccc cttgggtacc agaggaggct gtgcattgtg aataaagagt 1650
gagcttggt 1659

<210> 12
<211> 511
<212> PRT
<213> Homo sapiens

<400> 12

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Glu Glu Pro Pro Glu Glu Glu Ile Pro Lys Glu Asp Gly Ile Leu Val
20 25 30
Leu Ser Arg His Thr Leu Gly Leu Ala Leu Arg Glu His Pro Ala Leu
35 40 45
Leu Val Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Gln Ala Leu Ala
50 55 60
Pro Glu Tyr Ser Lys Ala Ala Ala Val Leu Ala Ala Glu Ser Met Val
65 70 75 80
Val Thr Leu Ala Lys Val Asp Gly Pro Ala Gln Arg Glu Leu Ala Glu
85 90 95
Glu Phe Gly Val Thr Glu Tyr Pro Thr Leu Lys Phe Phe Arg Asn Gly
100 105 110
Asn Arg Thr His Pro Glu Glu Tyr Thr Gly Pro Arg Asp Ala Glu Gly
115 120 125
Ile Ala Glu Trp Leu Arg Arg Arg Val Gly Pro Ser Ala Met Arg Leu
130 135 140
Glu Asp Glu Ala Ala Ala Gln Ala Leu Ile Gly Gly Arg Asp Leu Val
145 150 155 160
Val Ile Gly Phe Phe Gln Asp Leu Gln Asp Glu Asp Val Ala Thr Phe
165 170 175
Leu Ala Leu Ala Gln Asp Ala Leu Asp Met Thr Phe Gly Leu Thr Asp
180 185 190
Arg Pro Arg Leu Phe Gln Gln Phe Gly Leu Thr Lys Asp Thr Val Val
195 200 205
Leu Phe Lys Lys Phe Asp Glu Gly Arg Ala Asp Phe Pro Val Asp Glu
210 215 220
Glu Leu Gly Leu Asp Leu Gly Asp Leu Ser Arg Phe Leu Val Thr His
225 230 235 240

Ser Met Arg Leu Val Thr Glu Phe Asn Ser Gln Thr Ser Ala Lys Ile
 245 250 255
 Phe Ala Ala Arg Ile Leu Asn His Leu Leu Leu Phe Val Asn Gln Thr
 260 265 270
 Leu Ala Ala His Arg Glu Leu Leu Ala Gly Phe Gly Glu Ala Ala Pro
 275 280 285
 Arg Phe Arg Gly Gln Val Leu Phe Val Val Val Asp Val Ala Ala Asp
 290 295 300
 Asn Glu His Val Leu Gln Tyr Phe Gly Leu Lys Ala Glu Ala Ala Pro
 305 310 315 320
 Thr Leu Arg Leu Val Asn Leu Glu Thr Thr Lys Lys Tyr Ala Pro Val
 325 330 335
 Asp Gly Gly Pro Val Thr Ala Ala Ser Ile Thr Ala Phe Cys His Ala
 340 345 350
 Val Leu Asn Gly Gln Val Lys Pro Tyr Leu Leu Ser Gln Glu Ile Pro
 355 360 365
 Pro Asp Trp Asp Gln Arg Pro Val Lys Thr Leu Val Gly Lys Asn Phe
 370 375 380
 Glu Gln Val Ala Phe Asp Glu Thr Lys Asn Val Phe Val Lys Phe Tyr
 385 390 395 400
 Ala Pro Trp Cys Thr His Cys Lys Glu Met Ala Pro Ala Trp Glu Ala
 405 410 415
 Leu Ala Glu Lys Tyr Gln Asp His Glu Asp Ile Ile Ile Ala Glu Leu
 420 425 430
 Asp Ala Thr Ala Asn Glu Leu Asp Ala Phe Ala Val His Gly Phe Pro
 435 440 445
 Thr Leu Lys Tyr Phe Pro Ala Gly Pro Gly Arg Lys Val Ile Glu Tyr
 450 455 460
 Lys Ser Thr Arg Asp Leu Glu Thr Phe Ser Lys Phe Leu Asp Asn Gly
 465 470 475 480
 Gly Val Leu Pro Thr Glu Glu Ser Pro Glu Glu Pro Ala Ala Pro Phe
 485 490 495
 Pro Glu Pro Pro Ala Asn Ser Thr Met Gly Ser Lys Glu Glu Leu
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<210> 13

<211> 2865

<212> DNA

<213> Homo sapiens

<220>

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<222> (46)... (1980)

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 Met Arg Pro Arg
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aaa gcc ttc ctg ctc ctg ctg ctc ttg ggg ctg gtg cag ctg ctg gcc 105
 Lys Ala Phe Leu Leu Leu Leu Leu Gly Leu Val Gln Leu Leu Ala
 5 10 15 20

gtg gcg ggt gcc gag gcc ccg gac gag gat tct tct aac aga gaa aat 153
 Val Ala Gly Ala Glu Gly Pro Asp Glu Asp Ser Ser Asn Arg Glu Asn
 25 30 35

gcc att gag gat gaa gag gag gag gag gag gaa gat gat gat gag gaa 201
 Ala Ile Glu Asp Glu Glu Glu Glu Glu Glu Glu Asp Asp Asp Glu Glu
 40 45 50

gaa gac gac ttg gaa gtt aag gaa gaa aat gga gtc ttg gtc cta aat Glu Asp Asp Leu Glu Val Lys Glu Glu Asn Gly Val Leu Val Leu Asn 55 60 65	249
gat gca aac ttt gat aat ttt gtg gct gac aaa gac aca gtg ctg ctg Asp Ala Asn Phe Asp Asn Phe Val Ala Asp Lys Asp Thr Val Leu Leu 70 75 80	297
gag ttt tat gct cca tgg tgt gga cat tgc aag cag ttt gct ccg gaa Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Gln Phe Ala Pro Glu 85 90 95 100	345
tat gaa aaa att gcc aac ata tta aag gat aaa gat cct ccc att cct Tyr Glu Lys Ile Ala Asn Ile Leu Lys Asp Lys Asp Pro Pro Ile Pro 105 110 115	393
gtt gcc aag atc gat gca acc tca gcg tct gtg ctg gcc agc agg ttt Val Ala Lys Ile Asp Ala Thr Ser Ala Ser Val Leu Ala Ser Arg Phe 120 125 130	441
gat gtg agt ggc tac ccc acc atc aag atc ctt aag aag ggg cag gct Asp Val Ser Gly Tyr Pro Thr Ile Lys Ile Leu Lys Lys Gly Gln Ala 135 140 145	489
gta gac tac gag ggc tcc aga acc cag gaa gaa att gtt gcc aag gtc Val Asp Tyr Glu Gly Ser Arg Thr Gln Glu Glu Ile Val Ala Lys Val 150 155 160	537
aga gaa gtc tcc cag ccc gac tgg acg cct cca cca gaa gtc acg ctt Arg Glu Val Ser Gln Pro Asp Trp Thr Pro Pro Pro Glu Val Thr Leu 165 170 175 180	585
gtg ttg acc aaa gag aac ttt gat gaa gtt gtg aat gat gca gat atc Val Leu Thr Lys Glu Asn Phe Asp Glu Val Val Asn Asp Ala Asp Ile 185 190 195	633
att ctg gtg gag ttt tat gcc cca tgg tgt gga cac tgc aag aaa ctt Ile Leu Val Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Lys Leu 200 205 210	681
gcc ccc gag tat gag aag gcc gcc aag gag ctc agc aag cgt tct cct Ala Pro Glu Tyr Glu Lys Ala Ala Lys Glu Leu Ser Lys Arg Ser Pro 215 220 225	729
cca att ccc ctg gca aag gtc gac gcc acc gca gaa aca gac ctg gcc Pro Ile Pro Leu Ala Lys Val Asp Ala Thr Ala Glu Thr Asp Leu Ala 230 235 240	777
aag agg ttt gat gtc tct ggc tat ccc acc ctg aaa att ttc cgc aaa Lys Arg Phe Asp Val Ser Gly Tyr Pro Thr Leu Lys Ile Phe Arg Lys 245 250 255 260	825
gga agg cct tat gac tac aac ggc cca cga gaa aaa tat gga atc gtt Gly Arg Pro Tyr Asp Tyr Asn Gly Pro Arg Glu Lys Tyr Gly Ile Val 265 270 275	873
gat tac atg atc gag cag tcc ggg cct ccc tcc aag gag att ctg acc Asp Tyr Met Ile Glu Gln Ser Gly Pro Pro Ser Lys Glu Ile Leu Thr 280 285 290	921
ctg aag cag gtc cag gag ttc ctg aag gat gga gac gat gtc atc atc	969

Leu	Lys	Gln	Val	Gln	Glu	Phe	Leu	Lys	Asp	Gly	Asp	Asp	Val	Ile	Ile		
	295						300					305					
atc	ggg	gtc	ttt	aag	ggg	gag	agt	gac	cca	gcc	tac	cag	caa	tac	cag	1017	
Ile	Gly	Val	Phe	Lys	Gly	Glu	Ser	Asp	Pro	Ala	Tyr	Gln	Gln	Tyr	Gln		
	310					315					320						
gat	gcc	gct	aac	aac	ctg	aga	gaa	gat	tac	aaa	ttt	cac	cac	act	ttc	1065	
Asp	Ala	Ala	Asn	Asn	Leu	Arg	Glu	Asp	Tyr	Lys	Phe	His	His	Thr	Phe		
	325				330					335					340		
agc	aca	gaa	ata	gca	aag	ttc	ttg	aaa	gtc	tcc	cag	ggg	cag	ttg	gtt	1113	
Ser	Thr	Glu	Ile	Ala	Lys	Phe	Leu	Lys	Val	Ser	Gln	Gly	Gln	Leu	Val		
				345					350					355			
gta	atg	cag	cct	gag	aaa	ttc	cag	tcc	aag	tat	gag	ccc	cgg	agc	cac	1161	
Val	Met	Gln	Pro	Glu	Lys	Phe	Gln	Ser	Lys	Tyr	Glu	Pro	Arg	Ser	His		
			360					365					370				
atg	atg	gac	gtc	cag	ggc	tcc	acc	cag	gac	tcg	gcc	atc	aag	gac	ttc	1209	
Met	Met	Asp	Val	Gln	Gly	Ser	Thr	Gln	Asp	Ser	Ala	Ile	Lys	Asp	Phe		
		375					380					385					
gtg	ctg	aag	tac	gcc	ctg	ccc	ctg	gtt	ggc	cac	cgc	aag	gtg	tca	aac	1257	
Val	Leu	Lys	Tyr	Ala	Leu	Pro	Leu	Val	Gly	His	Arg	Lys	Val	Ser	Asn		
	390					395					400						
gat	gct	aag	cgc	tac	acc	agg	cgc	ccc	ctg	gtg	gtc	gtc	tac	tac	agt	1305	
Asp	Ala	Lys	Arg	Tyr	Thr	Arg	Arg	Pro	Leu	Val	Val	Val	Tyr	Tyr	Ser		
	405				410				415						420		
gtg	gac	ttc	agc	ttt	gat	tac	aga	gct	gca	act	cag	ttt	tgg	cgg	agc	1353	
Val	Asp	Phe	Ser	Phe	Asp	Tyr	Arg	Ala	Ala	Thr	Gln	Phe	Trp	Arg	Ser		
				425				430						435			
aaa	gtc	cta	gag	gtg	gcc	aag	gac	ttc	cct	gag	tac	acc	ttt	gcc	att	1401	
Lys	Val	Leu	Glu	Val	Ala	Lys	Asp	Phe	Pro	Glu	Tyr	Thr	Phe	Ala	Ile		
			440					445					450				
gcg	gac	gaa	gag	gac	tat	gct	ggg	gag	gtg	aag	gac	ctg	ggg	ctc	agc	1449	
Ala	Asp	Glu	Glu	Asp	Tyr	Ala	Gly	Glu	Val	Lys	Asp	Leu	Gly	Leu	Ser		
		455					460					465					
gag	agt	ggg	gag	gat	gtc	aat	gcc	gcc	atc	ctg	gac	gag	agt	ggg	aag	1497	
Glu	Ser	Gly	Glu	Asp	Val	Asn	Ala	Ala	Ile	Leu	Asp	Glu	Ser	Gly	Lys		
	470					475					480						
aag	ttc	gcc	atg	gag	cca	gag	gag	ttt	gac	tct	gac	acc	ctc	cgc	gag	1545	
Lys	Phe	Ala	Met	Glu	Pro	Glu	Glu	Phe	Asp	Ser	Asp	Thr	Leu	Arg	Glu		
	485				490				495						500		
ttt	gtc	act	gct	ttc	aaa	aaa	gga	aaa	ctg	aag	cca	gtc	atc	aaa	tcc	1593	
Phe	Val	Thr	Ala	Phe	Lys	Lys	Gly	Lys	Leu	Lys	Pro	Val	Ile	Lys	Ser		
				505					510					515			
cag	cca	gtg	ccc	aag	aac	aac	aag	gga	ccc	gtc	aag	gtc	gtg	gtg	gga	1641	
Gln	Pro	Val	Pro	Lys	Asn	Asn	Lys	Gly	Pro	Val	Lys	Val	Val	Val	Gly		
			520					525					530				
aag	acc	ttt	gac	tcc	att	gtg	atg	gac	ccc	aag	aag	gac	gtc	ctc	atc	1689	
Lys	Thr	Phe	Asp	Ser	Ile	Val	Met	Asp	Pro	Lys	Lys	Asp	Val	Leu	Ile		

535 540 545

gag ttc tac gcg cca tgg tgc ggg cac tgc aag cag cta gag ccc gtg 1737
 Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Gln Leu Glu Pro Val
 550 555 560

tac aac agc ctg gcc aag aag tac aag ggc caa aag ggc ctg gtc atc 1785
 Tyr Asn Ser Leu Ala Lys Lys Tyr Lys Gly Gln Lys Gly Leu Val Ile
 565 570 575 580

gcc aag atg gac gcc act gcc aac gac gtc ccc agc gac cgc tat aag 1833
 Ala Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser Asp Arg Tyr Lys
 585 590 595

gtg gag ggc ttc ccc acc atc tac ttc gcc ccc agt ggg gac aaa aag 1881
 Val Glu Gly Phe Pro Thr Ile Tyr Phe Ala Pro Ser Gly Asp Lys Lys
 600 605 610

aac cca gtt aaa ttt gag ggt gga gac aga gat ctg gag cat ttg agc 1929
 Asn Pro Val Lys Phe Glu Gly Gly Asp Arg Asp Leu Glu His Leu Ser
 615 620 625

aag ttt ata gaa gaa cat gcc aca aaa ctg agc agg acc aag gaa gag 1977
 Lys Phe Ile Glu Glu His Ala Thr Lys Leu Ser Arg Thr Lys Glu Glu
 630 635 640

ctt tgaaggcctg aggtctgcgg aaggtgggag gaggcagacg ccctgcgtgg 2030
 Leu
 645

cccatggtcg gggcggtccac cggaggccgg caacaaacga cagtatctcg gattcctttt 2090
 tttttttttt taatttttta tactttgttg tttcacttca tgctctgaat actgaataac 2150
 catgaatgac tgaatagttt agtccagatt tttacagagg atacatctat ttttatcatt 2210
 atttgggggt tgaaaaattt ttttttacac cttctaattt ctttatttct caaagcagat 2270
 aattcttctg tgtgaaaatg ttttcttttt ttaatttaag gtttaaaatt ccttttccaa 2330
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 agggctggga ccaaccgggt gagatccaca agtctctgga tgtggctgaa ggcaataca 2450
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 gcttctgtct ctagcccaag gaaagaccaa aacataggga aataaaagca tttatctttg 2570
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 <212> PRT
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 Gln Leu Leu Ala Val Ala Gly Ala Glu Gly Pro Asp Glu Asp Ser Ser
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 Asn Arg Glu Asn Ala Ile Glu Asp Glu Glu Glu Glu Glu Glu Glu Asp
 35 40 45
 Asp Asp Glu Glu Glu Asp Asp Leu Glu Val Lys Glu Glu Asn Gly Val
 50 55 60
 Leu Val Leu Asn Asp Ala Asn Phe Asp Asn Phe Val Ala Asp Lys Asp
 65 70 75 80

Thr Val Leu Leu Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Gln
 85 90 95
 Phe Ala Pro Glu Tyr Glu Lys Ile Ala Asn Ile Leu Lys Asp Lys Asp
 100 105 110
 Pro Pro Ile Pro Val Ala Lys Ile Asp Ala Thr Ser Ala Ser Val Leu
 115 120 125
 Ala Ser Arg Phe Asp Val Ser Gly Tyr Pro Thr Ile Lys Ile Leu Lys
 130 135 140
 Lys Gly Gln Ala Val Asp Tyr Glu Gly Ser Arg Thr Gln Glu Glu Ile
 145 150 155 160
 Val Ala Lys Val Arg Glu Val Ser Gln Pro Asp Trp Thr Pro Pro Pro
 165 170 175
 Glu Val Thr Leu Val Leu Thr Lys Glu Asn Phe Asp Glu Val Val Asn
 180 185 190
 Asp Ala Asp Ile Ile Leu Val Glu Phe Tyr Ala Pro Trp Cys Gly His
 195 200 205
 Cys Lys Lys Leu Ala Pro Glu Tyr Glu Lys Ala Ala Lys Glu Leu Ser
 210 215 220
 Lys Arg Ser Pro Pro Ile Pro Leu Ala Lys Val Asp Ala Thr Ala Glu
 225 230 235 240
 Thr Asp Leu Ala Lys Arg Phe Asp Val Ser Gly Tyr Pro Thr Leu Lys
 245 250 255
 Ile Phe Arg Lys Gly Arg Pro Tyr Asp Tyr Asn Gly Pro Arg Glu Lys
 260 265 270
 Tyr Gly Ile Val Asp Tyr Met Ile Glu Gln Ser Gly Pro Pro Ser Lys
 275 280 285
 Glu Ile Leu Thr Leu Lys Gln Val Gln Glu Phe Leu Lys Asp Gly Asp
 290 295 300
 Asp Val Ile Ile Ile Gly Val Phe Lys Gly Glu Ser Asp Pro Ala Tyr
 305 310 315 320
 Gln Gln Tyr Gln Asp Ala Ala Asn Asn Leu Arg Glu Asp Tyr Lys Phe
 325 330 335
 His His Thr Phe Ser Thr Glu Ile Ala Lys Phe Leu Lys Val Ser Gln
 340 345 350
 Gly Gln Leu Val Val Met Gln Pro Glu Lys Phe Gln Ser Lys Tyr Glu
 355 360 365
 Pro Arg Ser His Met Met Asp Val Gln Gly Ser Thr Gln Asp Ser Ala
 370 375 380
 Ile Lys Asp Phe Val Leu Lys Tyr Ala Leu Pro Leu Val Gly His Arg
 385 390 395 400
 Lys Val Ser Asn Asp Ala Lys Arg Tyr Thr Arg Arg Pro Leu Val Val
 405 410 415
 Val Tyr Tyr Ser Val Asp Phe Ser Phe Asp Tyr Arg Ala Ala Thr Gln
 420 425 430
 Phe Trp Arg Ser Lys Val Leu Glu Val Ala Lys Asp Phe Pro Glu Tyr
 435 440 445
 Thr Phe Ala Ile Ala Asp Glu Glu Asp Tyr Ala Gly Glu Val Lys Asp
 450 455 460
 Leu Gly Leu Ser Glu Ser Gly Glu Asp Val Asn Ala Ala Ile Leu Asp
 465 470 475 480
 Glu Ser Gly Lys Lys Phe Ala Met Glu Pro Glu Glu Phe Asp Ser Asp
 485 490 495
 Thr Leu Arg Glu Phe Val Thr Ala Phe Lys Lys Gly Lys Leu Lys Pro
 500 505 510
 Val Ile Lys Ser Gln Pro Val Pro Lys Asn Asn Lys Gly Pro Val Lys
 515 520 525
 Val Val Val Gly Lys Thr Phe Asp Ser Ile Val Met Asp Pro Lys Lys
 530 535 540
 Asp Val Leu Ile Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Gln
 545 550 555 560
 Leu Glu Pro Val Tyr Asn Ser Leu Ala Lys Lys Tyr Lys Gly Gln Lys

565 570 575
 Gly Leu Val Ile Ala Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser
 580 585 590
 Asp Arg Tyr Lys Val Glu Gly Phe Pro Thr Ile Tyr Phe Ala Pro Ser
 595 600 605
 Gly Asp Lys Lys Asn Pro Val Lys Phe Glu Gly Gly Asp Arg Asp Leu
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 645

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<220>
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 ggg tcg gtc aga gct gac gat gaa gtt gat gtg gat ggt aca gta gaa 96
 Gly Ser Val Arg Ala Asp Asp Glu Val Asp Val Asp Gly Thr Val Glu
 20 25 30
 gag gat ctg ggt aaa agt aga gaa gga tca agg acg gat gat gaa gta 144
 Glu Asp Leu Gly Lys Ser Arg Glu Gly Ser Arg Thr Asp Asp Glu Val
 35 40 45
 gta cag aga gag gaa gaa gct att cag ttg gat gga tta aat gca tca 192
 Val Gln Arg Glu Glu Glu Ala Ile Gln Leu Asp Gly Leu Asn Ala Ser
 50 55 60
 caa ata aga gaa ctt aga gag aag tcg gaa aag ttt gcc ttc caa gcc 240
 Gln Ile Arg Glu Leu Arg Glu Lys Ser Glu Lys Phe Ala Phe Gln Ala
 65 70 75 80
 gaa gtt aac aga atg atg aaa ctt atc atc aat tca ttg tat aaa aat 288
 Glu Val Asn Arg Met Met Lys Leu Ile Ile Asn Ser Leu Tyr Lys Asn
 85 90 95
 aaa gag att ttc ctg aga gaa ctg att tca aat gct tct gat gct tta 336
 Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu
 100 105 110
 gat aag ata agg cta ata tca ctg act gat gaa aat gct ctt tct gga 384
 Asp Lys Ile Arg Leu Ile Ser Leu Thr Asp Glu Asn Ala Leu Ser Gly
 115 120 125
 aat gag gaa cta aca gtc aaa att aag tgt gat aag gag aag aac ctg 432
 Asn Glu Glu Leu Thr Val Lys Ile Lys Cys Asp Lys Glu Lys Asn Leu
 130 135 140
 ctg cat gtc aca gac acc ggt gta gga atg acc aga gaa gag ttg gtt 480
 Leu His Val Thr Asp Thr Gly Val Gly Met Thr Arg Glu Glu Leu Val
 145 150 155 160

aaa aac ctt ggt acc ata gcc aaa tct ggg aca agc gag ttt tta aac Lys Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Ser Glu Phe Leu Asn 165 170 175	528
aaa atg act gaa gca cag gaa gat ggc cag tca act tct gaa ttg att Lys Met Thr Glu Ala Gln Glu Asp Gly Gln Ser Thr Ser Glu Leu Ile 180 185 190	576
ggc cag ttt ggt gtc ggt ttc tat tcc gcc ttc ctt gta gca gat aag Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala Asp Lys 195 200 205	624
gtt att gtc act tca aaa cac aac aac gat acc cag cac atc tgg gag Val Ile Val Thr Ser Lys His Asn Asn Asp Thr Gln His Ile Trp Glu 210 215 220	672
tct gac tcc aat gaa ttt tct gta att gct gac cca aga gga aac act Ser Asp Ser Asn Glu Phe Ser Val Ile Ala Asp Pro Arg Gly Asn Thr 225 230 235 240	720
cta gga cgg gga acg aca att acc ctt gtc tta aaa gaa gaa gca tct Leu Gly Arg Gly Thr Thr Ile Thr Leu Val Leu Lys Glu Glu Ala Ser 245 250 255	768
gat tac ctt gaa ttg gat aca att aaa aat ctc gtc aaa aaa tat tca Asp Tyr Leu Glu Leu Asp Thr Ile Lys Asn Leu Val Lys Lys Tyr Ser 260 265 270	816
cag ttc ata aac ttt cct att tat gta tgg agc agc aag act gaa act Gln Phe Ile Asn Phe Pro Ile Tyr Val Trp Ser Ser Lys Thr Glu Thr 275 280 285	864
gtt gag gag ccc atg gag gaa gaa gaa gca gcc aaa gaa gag aaa gaa Val Glu Glu Pro Met Glu Glu Glu Glu Ala Ala Lys Glu Glu Lys Glu 290 295 300	912
gaa tct gat gat gaa gct gca gta gag gaa gaa gaa gaa gaa aag aaa Glu Ser Asp Asp Glu Ala Val Glu Glu Glu Glu Glu Glu Lys Lys 305 310 315 320	960
cca aag act aaa aaa gtt gaa aaa act gtc tgg gac tgg gaa ctt atg Pro Lys Thr Lys Lys Val Glu Lys Thr Val Trp Asp Trp Glu Leu Met 325 330 335	1008
aat gat atc aaa cca ata tgg cag aga cca tca aaa gaa gta gaa gaa Asn Asp Ile Lys Pro Ile Trp Gln Arg Pro Ser Lys Glu Val Glu Glu 340 345 350	1056
gat gaa tac aaa gct ttc tac aaa tca ttt tca aag gaa agt gat gac Asp Glu Tyr Lys Ala Phe Tyr Lys Ser Phe Ser Lys Glu Ser Asp Asp 355 360 365	1104
ccc atg gct tat att cac ttt act gct gaa ggg gaa gtt acc ttc aaa Pro Met Ala Tyr Ile His Phe Thr Ala Glu Gly Glu Val Thr Phe Lys 370 375 380	1152
tca att tta ttt gta ccc aca tct gct cca cgt ggt ctg ttt gac gaa Ser Ile Leu Phe Val Pro Thr Ser Ala Pro Arg Gly Leu Phe Asp Glu 385 390 395 400	1200

tat gga tct aaa aag agc gat tac att aag ctc tat gtg cgc cgt gta Tyr Gly Ser Lys Lys Ser Asp Tyr Ile Lys Leu Tyr Val Arg Arg Val 405 410 415	1248
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gtc aag ggt gtg gtg gac tca gat gat ctc ccc ttg aat gtt tcc cgc Val Lys Gly Val Val Asp Ser Asp Asp Leu Pro Leu Asn Val Ser Arg 435 440 445	1344
gag act ctt cag caa cat aaa ctg ctt aag gtg att agg aag aag ctt Glu Thr Leu Gln Gln His Lys Leu Leu Lys Val Ile Arg Lys Lys Leu 450 455 460	1392
gtt cgt aaa acg ctg gac atg atc aag aag att gct gat gat aaa tac Val Arg Lys Thr Leu Asp Met Ile Lys Lys Ile Ala Asp Asp Lys Tyr 465 470 475 480	1440
aat gat act ttt tgg aaa gaa ttt ggt acc aac atc aag ctt ggt gtg Asn Asp Thr Phe Trp Lys Glu Phe Gly Thr Asn Ile Lys Leu Gly Val 485 490 495	1488
att gaa gac cac tcg aat cga aca cgt ctt gct aaa ctt ctt agg ttc Ile Glu Asp His Ser Asn Arg Thr Arg Leu Ala Lys Leu Leu Arg Phe 500 505 510	1536
cag tct tct cat cat cca act gac att act agc cta gac cag tat gtg Gln Ser Ser His His Pro Thr Asp Ile Thr Ser Leu Asp Gln Tyr Val 515 520 525	1584
gaa aga atg aag gaa aaa caa gac aaa atc tac ttc atg gct ggg tcc Glu Arg Met Lys Glu Lys Gln Asp Lys Ile Tyr Phe Met Ala Gly Ser 530 535 540	1632
agc aga aaa gag gct gaa tct tct cca ttt gtt gag cga ctt ctg aaa Ser Arg Lys Glu Ala Glu Ser Ser Pro Phe Val Glu Arg Leu Leu Lys 545 550 555 560	1680
aag ggc tat gaa gtt att tac ctc aca gaa cct gtg gat gaa tac tgt Lys Gly Tyr Glu Val Ile Tyr Leu Thr Glu Pro Val Asp Glu Tyr Cys 565 570 575	1728
att cag gcc ctt ccc gaa ttt gat ggg aag agg ttc cag aat gtt gcc Ile Gln Ala Leu Pro Glu Phe Asp Gly Lys Arg Phe Gln Asn Val Ala 580 585 590	1776
aag gaa gga gtg aag ttc gat gaa agt gag aaa act aag gag agt cgt Lys Glu Gly Val Lys Phe Asp Glu Ser Glu Lys Thr Lys Glu Ser Arg 595 600 605	1824
gaa gca gtt gag aaa gaa ttt gag cct ctg ctg aat tgg atg aaa gat Glu Ala Val Glu Lys Glu Phe Glu Pro Leu Leu Asn Trp Met Lys Asp 610 615 620	1872
aaa gcc ctt aag gac aag att gaa aag gct gtg gtg tct cag cgc ctg Lys Ala Leu Lys Asp Lys Ile Glu Lys Ala Val Val Ser Gln Arg Leu 625 630 635 640	1920
aca gaa tct ccg tgt gct ttg gtg gcc agc cag tac gga tgg tct ggc	1968

Thr	Glu	Ser	Pro	Cys	Ala	Leu	Val	Ala	Ser	Gln	Tyr	Gly	Trp	Ser	Gly		
				645					650					655			
aac	atg	gag	aga	atc	atg	aaa	gca	caa	gcg	tac	caa	acg	ggc	aag	gac		2016
Asn	Met	Glu	Arg	Ile	Met	Lys	Ala	Gln	Ala	Tyr	Gln	Thr	Gly	Lys	Asp		
			660					665					670				
atc	tct	aca	aat	tac	tat	gcg	agt	cag	aag	aaa	aca	ttt	gaa	att	aat		2064
Ile	Ser	Thr	Asn	Tyr	Tyr	Ala	Ser	Gln	Lys	Lys	Thr	Phe	Glu	Ile	Asn		
			675				680					685					
ccc	aga	cac	ccg	ctg	atc	aga	gac	atg	ctt	cga	cga	att	aag	gaa	gat		2112
Pro	Arg	His	Pro	Leu	Ile	Arg	Asp	Met	Leu	Arg	Arg	Ile	Lys	Glu	Asp		
			690				695				700						
gaa	gat	gat	aaa	aca	gtt	ttg	gat	ctt	gct	gtg	gtt	ttg	ttt	gaa	aca		2160
Glu	Asp	Asp	Lys	Thr	Val	Leu	Asp	Leu	Ala	Val	Val	Leu	Phe	Glu	Thr		
	705				710					715					720		
gca	acg	ctt	cgg	tca	ggg	tat	ctt	tta	cca	gac	act	aaa	gca	tat	gga		2208
Ala	Thr	Leu	Arg	Ser	Gly	Tyr	Leu	Leu	Pro	Asp	Thr	Lys	Ala	Tyr	Gly		
			725						730					735			
gat	aga	ata	gaa	aga	atg	ctt	cgc	ctc	agt	ttg	aac	att	gac	cct	gat		2256
Asp	Arg	Ile	Glu	Arg	Met	Leu	Arg	Leu	Ser	Leu	Asn	Ile	Asp	Pro	Asp		
			740					745					750				
gca	aag	gtg	gaa	gaa	gag	cct	gaa	gaa	gaa	cct	gaa	gag	aca	gca	gaa		2304
Ala	Lys	Val	Glu	Glu	Glu	Pro	Glu	Glu	Glu	Pro	Glu	Glu	Thr	Ala	Glu		
		755					760					765					
gac	aca	aca	gaa	gac	aca	gag	caa	gac	gaa	gat	gaa	gaa	atg	gat	gtg		2352
Asp	Thr	Thr	Glu	Asp	Thr	Glu	Gln	Asp	Glu	Asp	Glu	Glu	Met	Asp	Val		
		770				775					780						
gga	aca	gat	gaa	gaa	gaa	gaa	aca	gca	aag	gaa	tct	aca	gct	gaa	aaa		2400
Gly	Thr	Asp	Glu	Glu	Glu	Glu	Thr	Ala	Lys	Glu	Ser	Thr	Ala	Glu	Lys		
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gat	gaa	ttg	taa														2412
Asp	Glu	Leu															

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<211> 803

<212> PRT

<213> Homo sapiens

<400> 16

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Gly	Ser	Val	Arg	Ala	Asp	Asp	Glu	Val	Asp	Val	Asp	Gly	Thr	Val	Glu		
		20					25						30				
Glu	Asp	Leu	Gly	Lys	Ser	Arg	Glu	Gly	Ser	Arg	Thr	Asp	Asp	Glu	Val		
		35					40					45					
Val	Gln	Arg	Glu	Glu	Glu	Ala	Ile	Gln	Leu	Asp	Gly	Leu	Asn	Ala	Ser		
		50				55					60						
Gln	Ile	Arg	Glu	Leu	Arg	Glu	Lys	Ser	Glu	Lys	Phe	Ala	Phe	Gln	Ala		
		65			70				75					80			
Glu	Val	Asn	Arg	Met	Met	Lys	Leu	Ile	Ile	Asn	Ser	Leu	Tyr	Lys	Asn		

29/30

Ile Gln Ala Leu Pro Glu Phe Asp Gly Lys Arg Phe Gln Asn Val Ala
 580 585 590
 Lys Glu Gly Val Lys Phe Asp Glu Ser Glu Lys Thr Lys Glu Ser Arg
 595 600 605
 Glu Ala Val Glu Lys Glu Phe Glu Pro Leu Leu Asn Trp Met Lys Asp
 610 615 620
 Lys Ala Leu Lys Asp Lys Ile Glu Lys Ala Val Val Ser Gln Arg Leu
 625 630 635 640
 Thr Glu Ser Pro Cys Ala Leu Val Ala Ser Gln Tyr Gly Trp Ser Gly
 645 650 655
 Asn Met Glu Arg Ile Met Lys Ala Gln Ala Tyr Gln Thr Gly Lys Asp
 660 665 670
 Ile Ser Thr Asn Tyr Tyr Ala Ser Gln Lys Lys Thr Phe Glu Ile Asn
 675 680 685
 Pro Arg His Pro Leu Ile Arg Asp Met Leu Arg Arg Ile Lys Glu Asp
 690 695 700
 Glu Asp Asp Lys Thr Val Leu Asp Leu Ala Val Val Leu Phe Glu Thr
 705 710 715 720
 Ala Thr Leu Arg Ser Gly Tyr Leu Leu Pro Asp Thr Lys Ala Tyr Gly
 725 730 735
 Asp Arg Ile Glu Arg Met Leu Arg Leu Ser Leu Asn Ile Asp Pro Asp
 740 745 750
 Ala Lys Val Glu Glu Glu Pro Glu Glu Glu Pro Glu Glu Thr Ala Glu
 755 760 765
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<212> DNA

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<400> 17

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21